

FIG. 1

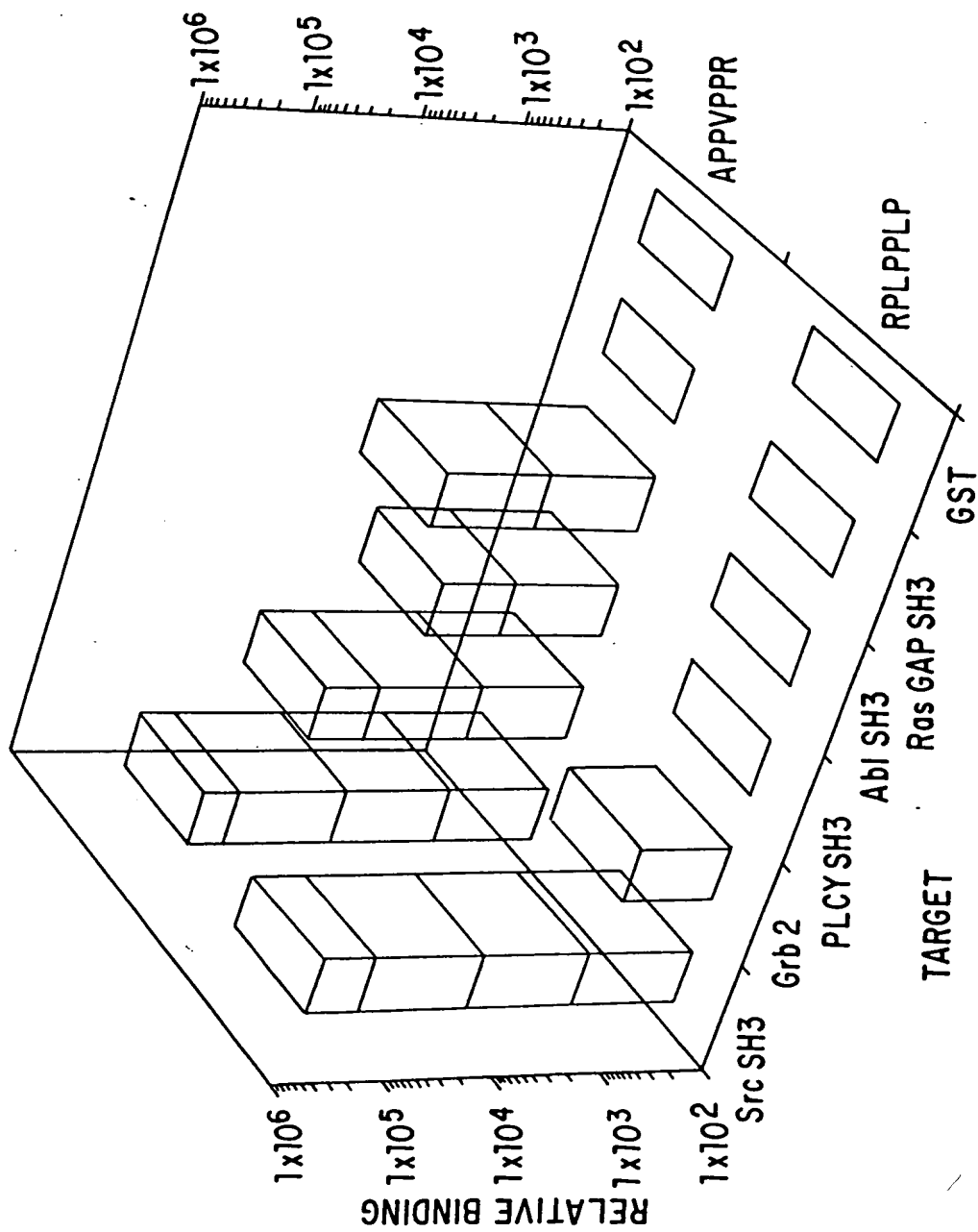


FIG. 2

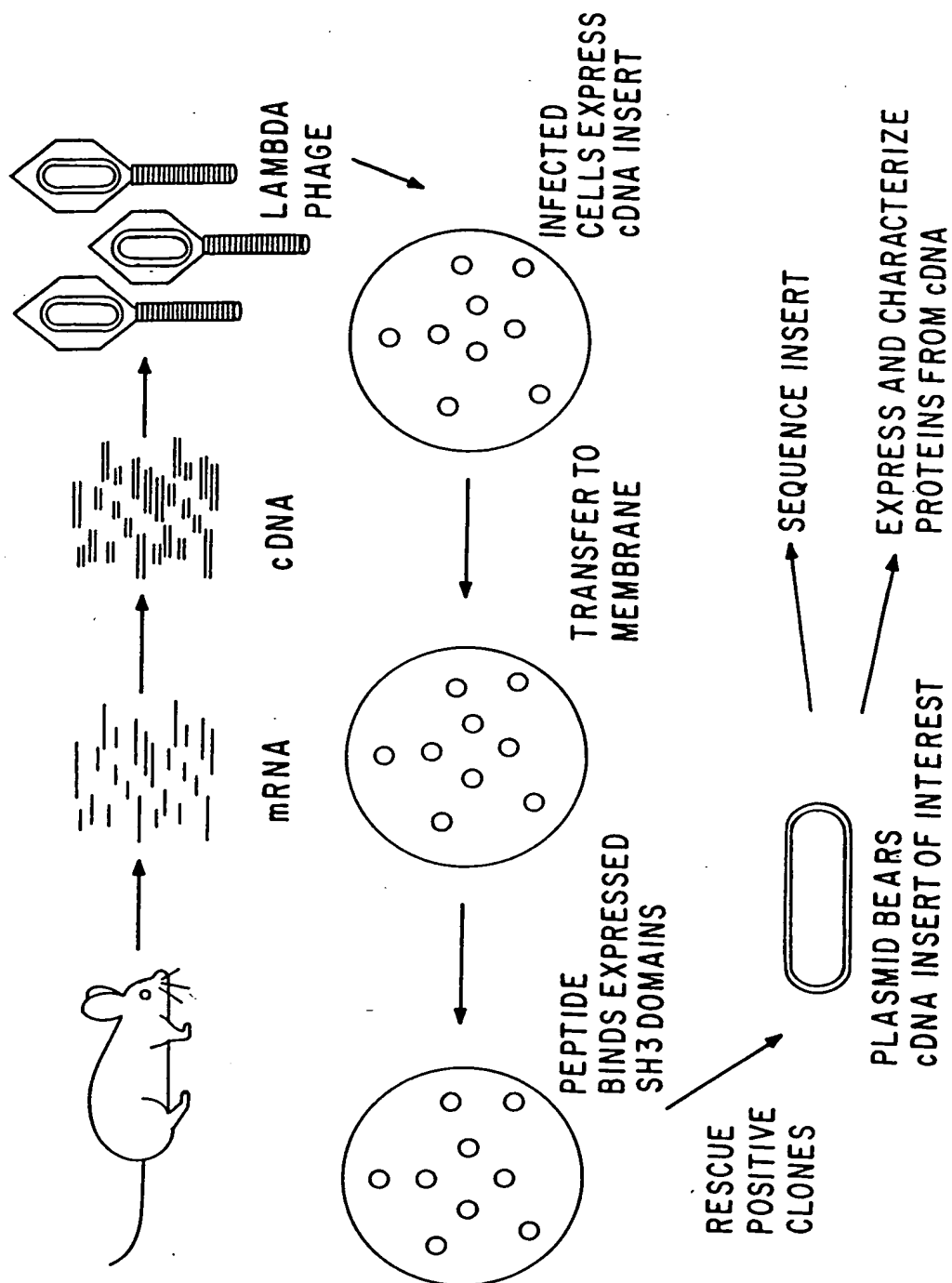


FIG. 3

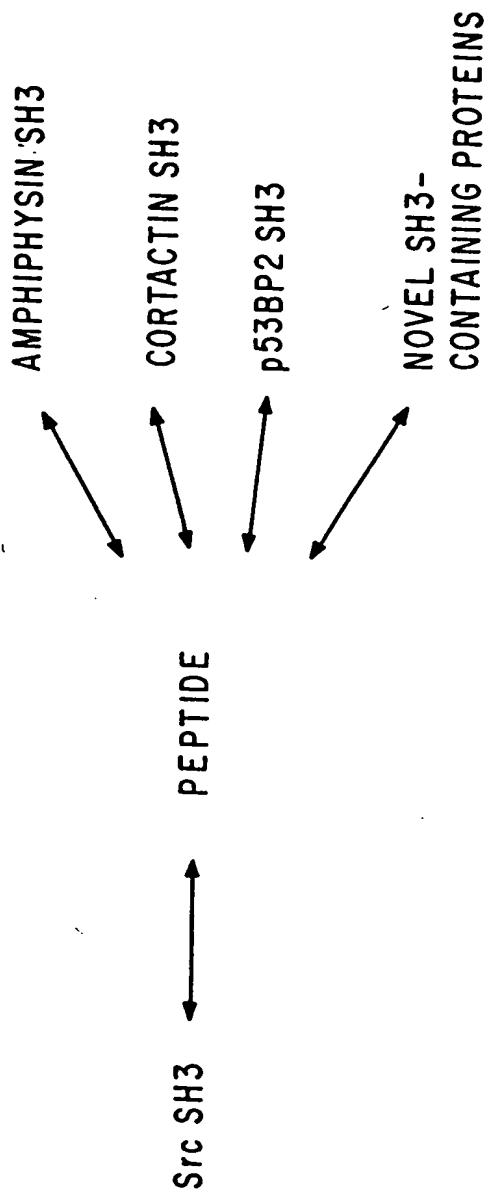


FIG. 4

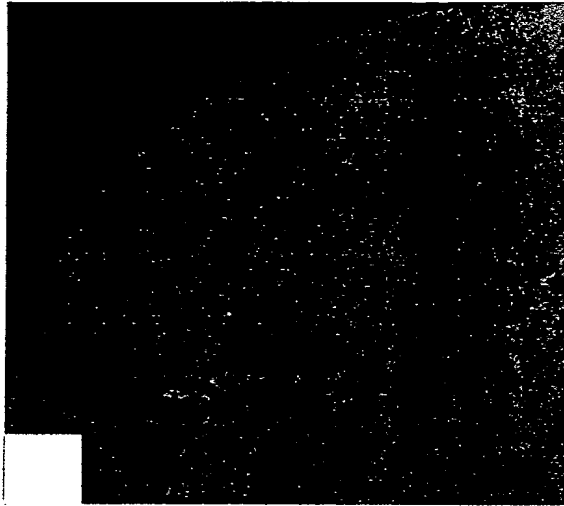


FIG. 5A

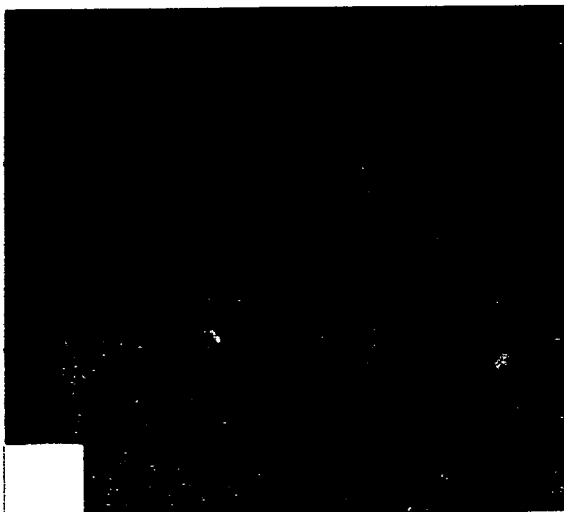


FIG. 5B

Sc_Fus1_Sh3:	TVI	QDYE	PRLTDE	IRISLG	EKVKIL	...A	THTD	CLVEKCNRK68
Sc_Bob1_Sh3:	RAL	FDYD	KTKDCGFLSQ	ALSFRFG	DVLHVIDA	GDEE	QAR RVHSDSE69
Hs_Mpp1_Sh3:	RAQ	FDYD	PKKONLIPCK	EAGLKFBATG	DIIOIINK	DDSN	QGR ..VEGSS70
Hs_Zo1_Sh3:	RTH	PHYE	KESPY	GLSFNKG	EVFRAVDTLY	NGKLG	AI RIGKNHKE71
Hs_Ncf1_Csh3:	VAI	KAYT	AV.EGD	..E.	VSLEGE	EAVEIVHK	LLDG	V IRKDDVTGY72
Hs_Rasgap_Sh3:	RAI	LPYT	KVPDID	..E.	ISFLKG	DMFIVHNE	LED	.. MIVTNLRT73
Sc_Sla_Nsh3:	RAV	YAYE	..PQTP	..EE	LAIQED	DLLYLLQKSD	IDD	TVKKR VIGSD74
Sc_Bem1_Nsh3:	KAK	YSYQ	..AQTS	..KE	LSFMGE	EFFYV	..SGD	EKD	KASNP STGKE75
Hs_Ncf2_Nsh3:	AHR	VLFG	FVPETK	..EE	LQWMPG	NIVFVL	..KK	GND	ATVMFNG.QK76
Sc_Sla_Csh3:	RGI	VQYD	FMAESQ	..DE	LTIKSG	DKVYLLDDKK	SKD	MCQLVDS.GK77
Hs_Grb2_Csh3:	QAL	FDPD	..PQED	..GE	LGFRRG	DFIHWMD	..N	S....	DPN	KG.A.CH.GQ78
Hs_Nck_Csh3:	QAL	YPFS	..SSND	..EE	LNFEKG	DVMDVIEKPE	..N	DPE	KCRK.IN.GM79
Mm_Tec_Sh3:	VAM	YDFG	..ATEA	..HD	RLRERG	QEYIILEKN	DLH	RARD.KN.GQ80
Hs_Atk_Sh3:	VAL	YDYN	..PMNA	..ND	LQLRKG	DEYFILEES	NLP	RARD.KY.GW81
Hs_Ab1_Sh3:	VAL	YDFV	..ASGD	..NT	LSITKG	EKLRLVGN	HNGE	EAQT.KN.GQ82
Hs_Src_Sh3:	VAL	YDYE	..SRTE	..TD	LSFKKG	ERLQIWNNT	EGD	LAHSLT.GQ83
Hs_Fgr_Sh3:	IAL	YDYE	..ARTE	..DD	LTFTKG	EKFHILNNT	EGD	EAPSLSS.GK84
Hs_Fyn_Sh3:	VAL	YDYE	..ARTE	..DD	LSFHKG	EKFQILNSS	EGD	EAPSLTT.GE85
Hs_Yes_Sh3:	VAL	YDYE	..ARTT	..ED	LSFKKG	ERFQIINNT	EGD	EARSAT.GK86
Mm_Fgr_Sh3:	VAL	YDYE	..ARTG	..DD	LTFTKG	EKFHILNNT	EYD	EAPSLSS.GH87
Hv_Stk_Sh3:	VAL	YDYE	..ARIS	..ED	LSFKKG	ERLQIINTA	DGD	YAPSLIT.NS88
Hs_Hck_Sh3:	VAL	YDYE	..AIHH	..ED	LSFOKG	QDMVVEES	GE	KARSLAT.RK89
Hs_Lyn_Sh3:	VAL	YPVD	..GIHP	..DD	LSFKKG	EKMKVLEEH	GE	KAKSLLT.KK90
Mm_Btk_Sh3:	VAL	PDYA	..AVND	..RD	LQVLKG	EKLQVLRST	GD	LARSLVT.GR91
Hs_Lck_Sh3:	IAL	HSYE	..PSHD	..GD	LGFEKG	EQLRILEQS	GE	KAQSLTT.GQ92
Hs_Nck_Nsh3:	VAK	FDYV	..AQQE	..QE	LOIKKN	ERLWLLDDSK	Sw	VRNSM...NK93	
Sc_Sla_Msh3:	RAI	YDYE	QVQNAD	..EE	LTTHEN	DVDFVFKD	DAD	LVKSTVS.NE94

FIG. 6A

Hs_Hs1_Sh3:	VAL YDQ	..GEGS..DELSFDPD DVITDIEMV.DEG	RG..RCH.GH95
Sc_Abp1_Sh3:	TAE YDYD	..AAED..NELTFVEN DKINIEFV.DDD	LGELEKD.GS96
Hs_Nck_Msh3:	YVK FNYN	..AERE..DELSLKG TKIVMEKC.SDG	RG..SYN.GQ97
Hs_Vav_Sh3:	KAR YDFC	..ARDR..SELSLKEG DIILNKK.GQQ	WRGEIY..GR98
Hs_Grb2_Nsh3:	IAK YDFK	..ATAD..DELSFKRG DILKVLNEE.CDQ	YKAELN..GK99
Hs_P1cg2_Sh3:	KAL YDYK	..AKRS..DELSFCRG ALIHNSKEPG	WKGDTGT.RI100
Hs_P1cg1_Sh3:	KAL FDYK	..AORE..DELTFIKS AIIONVEKQ.EG	WRGDYGG.KK101
Ac_Mys1b_Sh3:	KAL YDYD	..AQTG..DELTFKEG DTIIVHQKD.PA	WEGELN..GK102
Ac_Mys1c_Sh3:	RAL YDFA	..AENP..DELTFNEG AVTVINKS.NP	WEGELN..GQ103
Dd_Mys1b_Sh3:	KAL YDYD	..ASST..DELSFKEG DIIFIVQKD.NG	TQGELKS.GQ104
Hs_Ncf2_Csh3:	EAL FSYE	..ATQP..EDLEFQEG DIILVLSKV.NE	LEGECK..GK105
Hs_Ncf1_Nsh3:	RAI ADYE	..KTSG..SEMALSTG DVVEVVEKS.ESG	FCQM..K.AK106
Hs_Spectrin_Sh3:	MAL VDFQ	..ARSP..REVTMKG DVLTLSSI.NKD	KVEA..A.DH107
Sc_Bem1_Csh3:	YAI VLYD	FKAKEA..DELTTYVG ENLFICAH..HNCE	IAKPIGRLGG108
Sc_Cde25_Sh3:	VAA YDFN	YPIKKD..SS	..SQLLSVQQG ETIYILNKNS	SG	...DGL VIDD109
Sp_Ste_Sh3:	.MR FQTT	AISDYENSSN	.PSFLKFSAG DTIIVIEVLE	D	CDG.....110
Hs_Pf3ka_Sh3:	RAL VDYK	KEREEDIDLH	LGDILTVNKG SLVALGFSDG QEARPEEI		LNGYNETTGE111

FIG. 6B

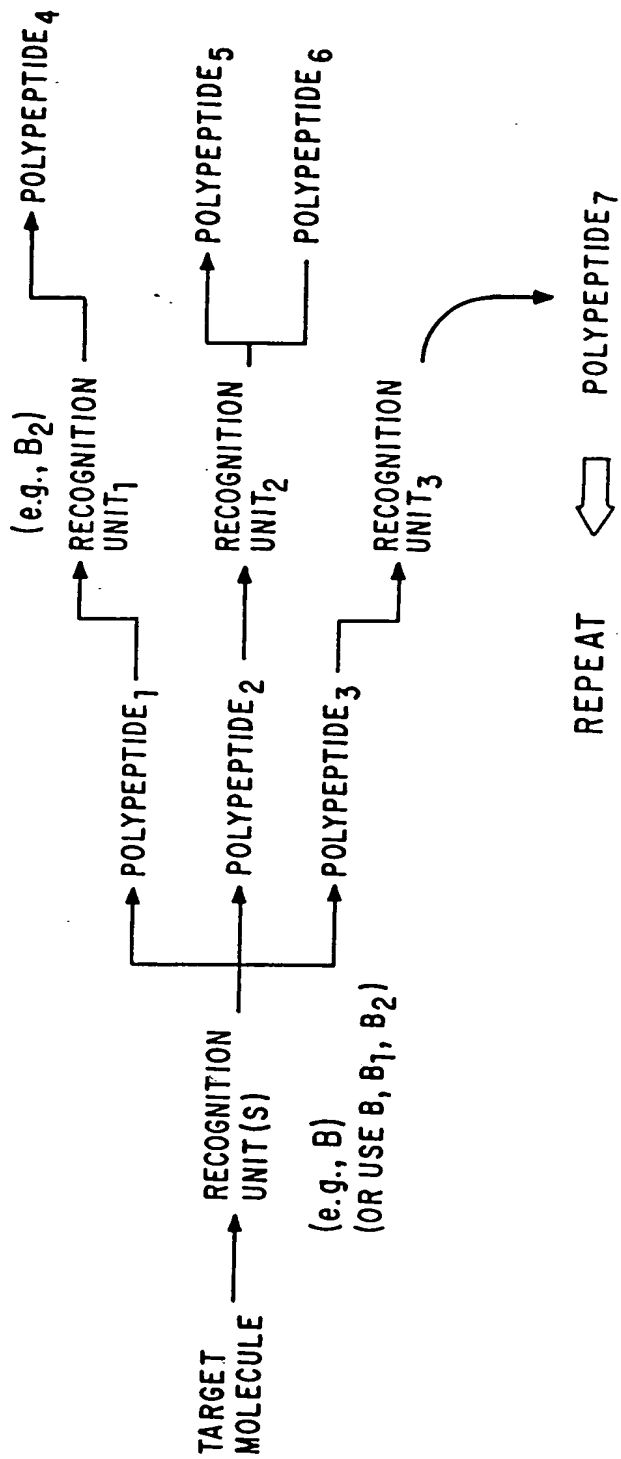


FIG. 7B

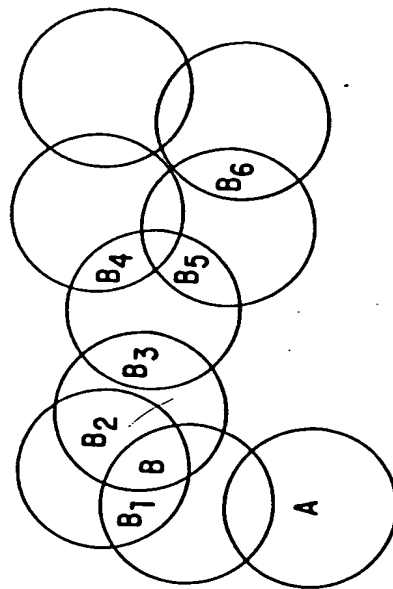


FIG. 7A

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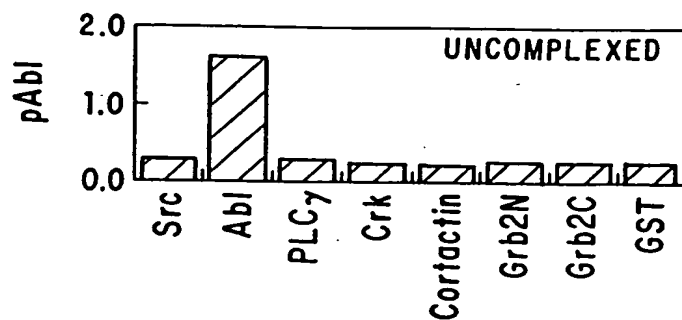


FIG. 8A

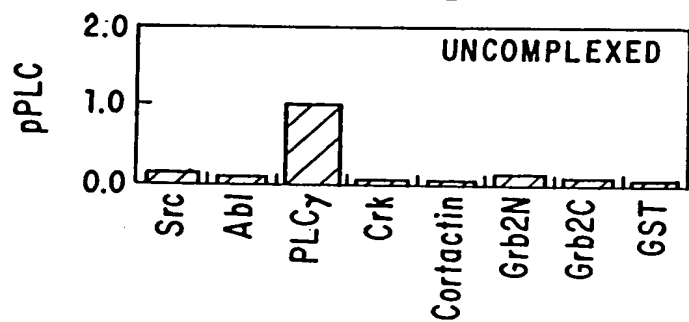


FIG. 8B

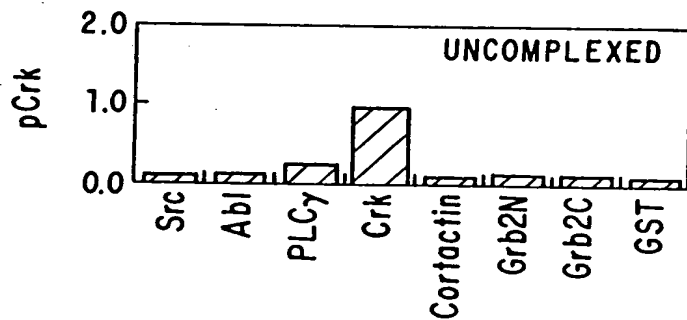


FIG. 8C

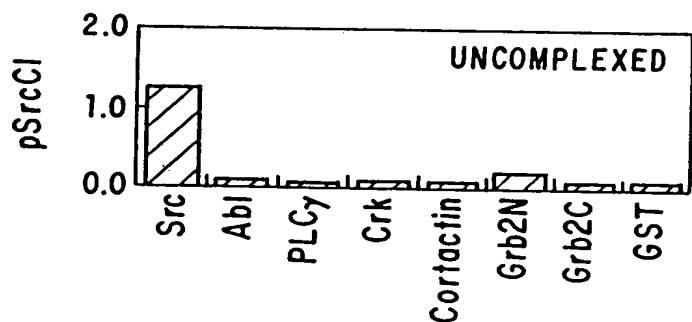


FIG. 8D

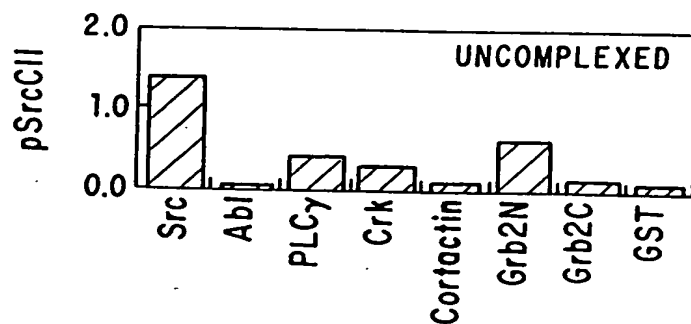


FIG. 8E

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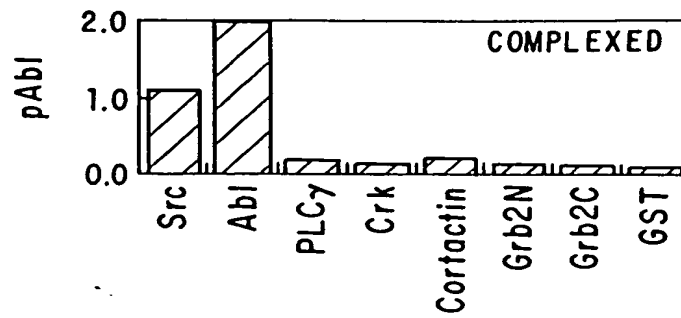


FIG. 8F

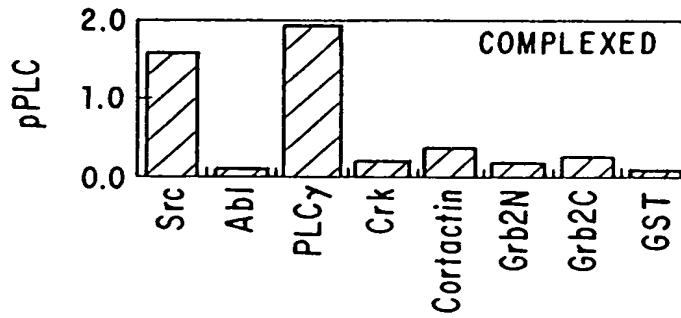


FIG. 8G

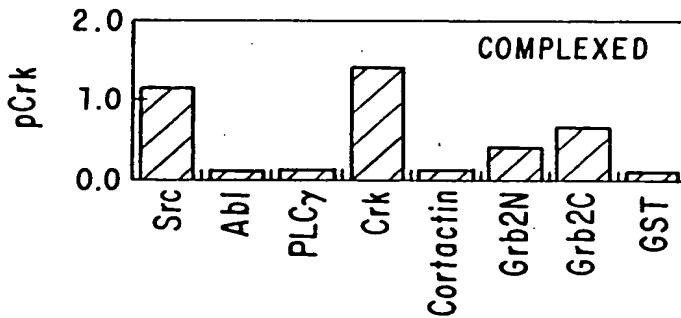


FIG. 8H

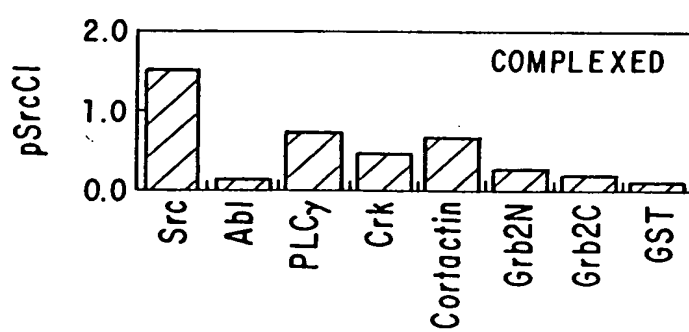


FIG. 8I

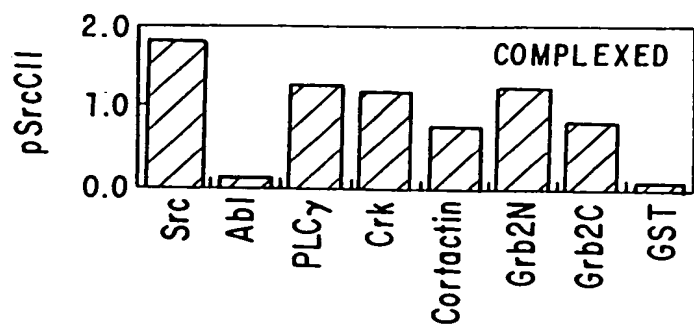


FIG. 8J

LIGAND: pSrcCII pCort pSrcCII pSrcCII
 LIBRARY: Mouse Human Human 2

NAME	IDENTITY	#CLONES
SH3P1	ARAR SH3	1
SH3P2	SH3P2 Novel	1
SH3P3	SH3	1
SH3P4	SH3	1
SH3P5	SH3P5 Cortactin	2
SH3P6	SH3P6 MLN50	1
SH3P7	SH3P7 Novel	1
SH3P8	SH3P8 Novel	1
SH3P9	SH3P9 Novel	9
SH3P10	SH3P10 HSI	1
SH3P11	SH3P11 Crk	2
SH3P12	SH3P12 Novel	1
SH3P13	SH3P13 Novel	2
SH3P14	SH3P14 H74	8
SH3P15	SH3P15 Lyn	1
SH3P16	SH3P16 Fyn	2
SH3P17	SH3P17 Novel	1
SH3P18	SH3P18 Novel	2

FIG. 9

SEQ. ID NO

SH3P1	p53bp2	NKGTVALWDYEAQNSDELSFHGDAITILRRKDN.....	ETEMMARLG.....	DREGVVPKNLLGLY.....	112
SH3P2	Novel	QVKVFRALYTFEPRTPDELYFEEDGIIYITMS.....	DTSWKGTKC.....	GRTGLIPSNYVAEQ.....	113
SH3P3	Novel	HWTPYRMYQYRPQNEDELELREGDRVDVWQC.....	DDGWFVGSRRT.....	QKFGTFPGNYVAPV.....	114
SH3P4	Novel	DQPCKALYDFEPENDGELGFREGDLITLTNQI.....	DENWYEGMLH.....	GQSGFFPLSYVQVL.....	115
SH3P5	Cortactin	LGITAIALYDYQAAGDDEISFDPPDDIITNIEMI.....	DDGMRGVCK.....	GRYGLFPANYVELR.....	116
SH3P6	MLN50	GGKRYRAVYDYSAADEDEVSFDQDITVNVQQI.....	DDGMYGTVERT.....	GDTGMLPANYVEAI.....	117
SH3P7	Novel	QGLCARALYDYQAADDTISFDPENLITGIEVI.....	DEGMRGYGPD.....	GHEGMPFANYVELI.....	118
SH3P8	Novel	DQPCCRALYDLEPENEGELAFKEGDIITLTNQI.....	DENWYEGMLH.....	GQSGFFPINYVEIL.....	119
SH3P9	Novel, m	FMFKVQAQHDYATATDDELQKAGDVVLVTFQNPPEEQDEGMLMGVKESDWNQHKLEKCRGVFPENFTERV.....			120
	Novel, h	FMFKVQAQHDYATATDDELQKAGDVVLVTFQNPPEEQDEGMLMGVKESDWNQHKLEKCRGVFPENFTERV.....			121
SH3P10	HS1	AGISAIALYDYQGESELSFDPDDIITDIEMV.....	DEGMRGQCR.....	GHFGLFPANYVKLL.....	122
SH3P11	Crk A	EAELYRALDFNGNDEEDLPFKKGDIILTRDKP.....	EEQWNAEDSE.....	GKRGMPVPYVEKY.....	123
	B	RVIQKRVPNAYDKTALALEVGELVKVTKINV.....	SGQWEGECN.....	GKRGHFFTHVRL.....	124
SH3P12	Novel A	EMRPARAKFDFAQTLKELPLQKGDVVYIRQI.....	DQNWYEGEHH.....	GRVGIFPRTYIELL.....	125
	B	EYGEATAKFNFGDTQVEMSFRKGERITLLRQV.....	DENWYEGRIPGT.....	SROGIFPITYVDVL.....	126
	C	DLCYQALYSYVPQNDDELELRGDIVDMKEC.....	DDGWFVGTSSRT.....	ROFGTFPGNYVKPL.....	127
SH3P13	Novel	DQPCCRGLYDFEPENEGELGFKEGDIITLTNQI.....	DENWYEGMLR.....	GESGFFPINYVEVI.....	128
SH3P14	H74, m	TEVRVRALDYEGQEHDELSFKAGDELTKMEDE.....	EQWCKGRLDN.....	GQVGLYPANYVEAI.....	129
	H74, h	KGVRVRALYDYGQEQDELSFKAGDELTKLGEED.....	EQWCRGRLDS.....	GQLGLYPANYVEAI.....	130
SH3P15	Lyn	QGDIVVALYPYDGIHPDDLFSKKGEKMKVLEE.....	HGEWMAKSLLT.....	KKEGFIPSNYVAKL.....	131
SH3P16	Fyn	GVTLFVALDYEARTEDDLFSHKGEKFQILNSS.....	EGDWMEARSLTT.....	GETGYIPSNYVAPV.....	132
SH3P17	Novel A	KVVYVRALYPFESRSHDEITIQPGDIVMDESQTG.....	EPGMLGGELK.....	GKTGMFPANYAEKI.....	133
	B	EGLQAQALYPWRACKDNHLNFKNDVITVLEQ.....	QDMWVFGEVQ.....	GQKGMFPKSYVKLI.....	134
	C	GEEIAQVIASYTATGPEQLTAPGQLILTRKKN.....	PGGWEGELQARGKK.....	ROIGMFPANYVKLL.....	135
	D	AVCQVIAMYDYTAQNDDDELAFNKGQIINVLNKE.....	DPDWMKGEVN.....	GQVGLFPSNYVKLT.....	136

FIG. 10A

SEQ. ID NO.

SH3P18 Nove1 B VGEYIALPYSSVEPGDLTFTEGEEILVTQK.....DGEMMTGSIG.....DRSGIFPSNYVKPK137
C KPEIAQVTSAYVAGSEQLSLAPGQLILILKKN.....TSGMWGELQARGKK.....RQKGMFPAASYVKLL138
D PVCQVIGMYDYAANNEDELSFSKGQLINVMNKD.....DPDMNQGEIN.....GVTGLFPSNYVLEE139
Src GVTTFVALYDYESRTETDLSFKKGERLQIVNNT.....EGDMWLAHSLTT.....GQTGYIPSNYVAPS140

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FIG. 10B

					SEQ. ID NO.
CLONE 5 P3-6		QVKVFRALYTFEPRTDPELYFEEDGIIYITDM	DTNWKGTG	GRTGLIPSNYVAEQ204
CLONE 34 Crk LIKE		TGEEYIAGDFTAQVGDITFKKGEILLVIEKK	PDGWIADAK	GNEGLVPRTYLEPY205
CLONE 40 Ab1 BINDING		YLEKVAIYDYTKOKEDELSFQEGAIIVIKKN	DDGWYEGVMN	GVTGLSPGNVYESI206
		PROTEIN			
CLONE 41 Nck LIKE A		LNIPAFVKFAYVAIEREDELVLKGSRTVMKEC	SDGWRGSGN	GQIGWFPSNVYLEE207
	Nck LIKE B	VLHVQTLYPFSSVTEELNEFEKGETMEVIEKPENDPEWVKCKNAR		GOVGLVPKNYVVVL208
CLONE 45 Nck A		EEVWVAKFDYVAQQEQELDIKKNERLWLLDD	SKSWVRVNSM	NKTGFVPSNVERK209
	Nck B	LNMPAYVKFNMAEREDELSLIKGTKVIVMEKIC	SDGWRGSGN	GQVGWFPSNVYTEE210
	Nck C	VLHVQALYPFSSNDEELNFEKGDVMDVIEKPEN	DPEWVKCRKIN	GMVGLVPKNYVTVM211
CLONE 53 NAB		DLFSYQALYSYIPQNDDELELRDGDIVDVMEKC	DDGWFVGTSRRT	KQFGTFPGNVKPL212
CLONE 55 NOVEL		QGRKERARYOLEAAQDNELTFKAGEIMTVLDDS	DPNWKGETH	QGIGLFPSNFVTAD213
CLONE 56 NOVEL		QGLCARALYDYQAADDTESISFDPENLITGIEVI	DEGWRGYGPD	GHFGMFPAHYVELI214
CLONE 65 NOVEL	A	VLVNRALYPFEARNHDEMFSNGDIIQVDEKTVG	EPGWL YGSFQ	GNFGWFPNHYVEKM215
	B	VENLKAQALCSWTAKK DNHLNFSKHDIITVLEQQ	ENFWWFGEVH	GGRGMFPKSYVKII216
	C	VGEYIALYPYSSVEPGDLTFTEGEEILVTQK	DGEWWTGSIG	DRSGIFPSNHYVKPK217
	D	KPEIAQVTSAYVASGS EQLSLAPGQLILILKKN	TSGWVQGELQARGKKRQKGMFPASWVKLL	218
	E	PVCQVIAMYDYAANNEDELVSFSGQLINVMNKD	DPDWVQGEIN	GVTGLFPSNHYVKMT219

FIG. 10C

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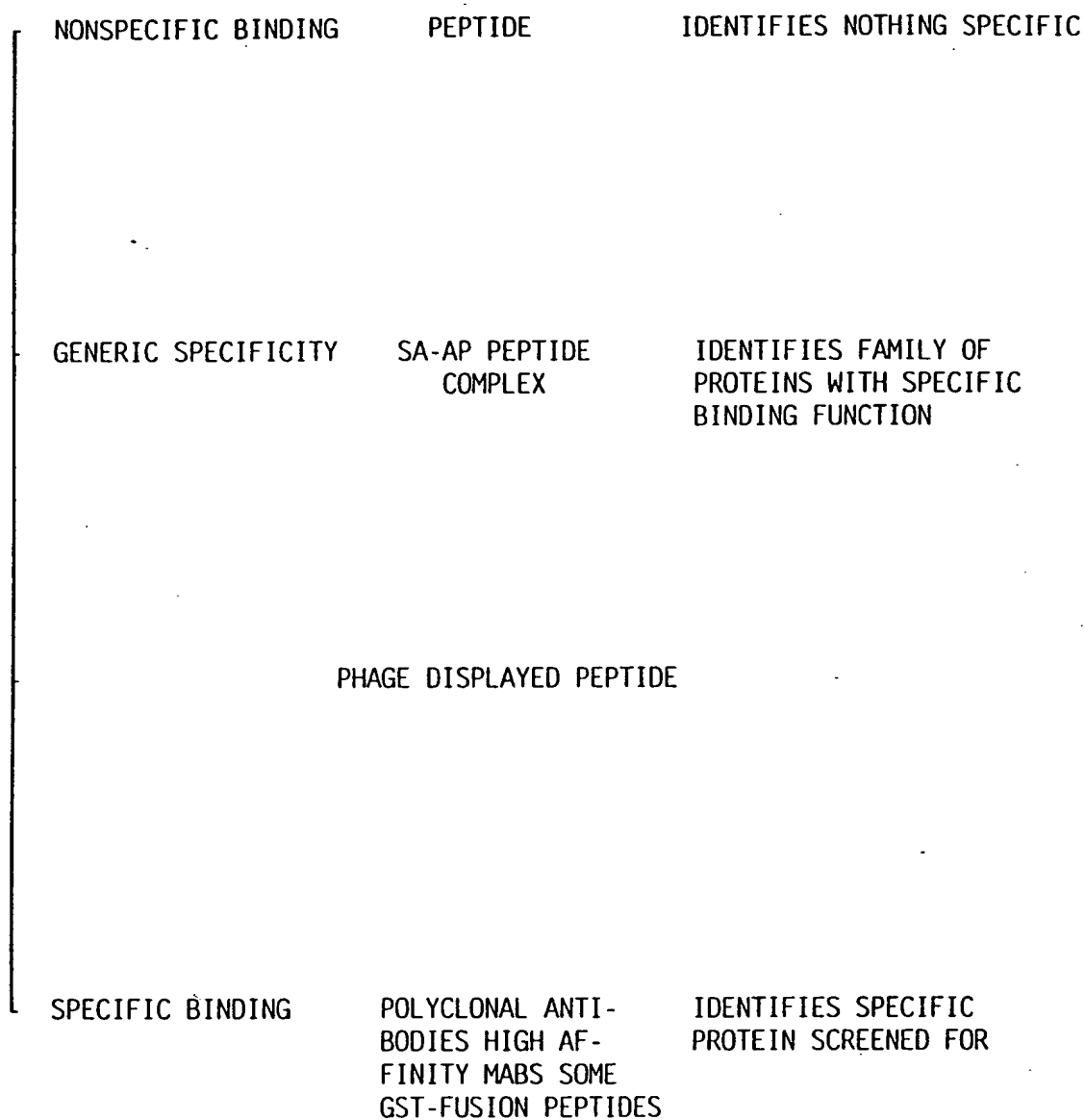


FIG. 11

SH3 DOMAIN CLONES																	
PEPTIDE	NAME	SEQUENCE	SEQ. ID NO.	5	11	12	13	14	18	34	40	41	45	46	53	55	65
SH3001	WBP-1	PGTPPPPYTVGPGY	141	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TPPY	WBP-1	HGTPPPPYTVGP	142	-	-	-	-	-	-	-	-	-	-	-	-	-	-
QPPY	WBP-2	YVQPPPPPYPCPM	143	-	-	-	-	-	-	-	-	-	-	-	-	-	-
YPPE	WBP-2	PGYPYPPPEFY	144	-	-	-	-	-	-	-	-	-	-	-	-	-	-
WW005	WBP-1	PGTPAPPYTVGPGY	145	-	-	-	-	-	-	-	-	-	-	-	-	-	-
WW006	WBP-1	PGTPAPPYTVGPGY	146	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3002	K+ CHANNEL	DSGVRPLPPLPDGV	147	-	-	-	+	+	-	++	-	-	-	-	-	-	-
bSH3003	K+ CHANNEL	VRPLPPLPEELPRRRPPPED	148	-	-	+	+	+	-	++	-	-	-	-	-	-	-
bSH3004	M4 AChr	PPPALPPPPRPVADK	149	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3005	β 1 ADRENERGIC	APAPPPGPPAAAA	150	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3006	RasGap	GGGFPLPPPPYLPPLG	151	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3007	MEK	SISPRRRPPGRPVSG	152	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3008	P Tyr PHOSP.	PPPEHI PPPPRKRILE	153	-	-	+	-	-	++	-	+	-	-	-	-	-	-
bSH3009	Fak	KEGERALPSIPKLAN	154	-	-	-	+	+	-	-	-	-	-	-	-	-	-
bSH3010	c-AbI	SRLKPAPPPPPAASAG	155	-	-	-	-	-	+++	-	-	-	-	-	-	-	-
bSH3011	c-Cbl	QASLPVPPRDLLLP	156	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3012	c-Cbl	PVPPTLRDLPPPPPPDRPYS	157	-	-	+++	++	++	-	+	-	-	-	-	-	-	-
bSH3013	Ca2+ CHANNEL	SDGGRNLPGTPVPAS	158	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3014	Ca2+ CHANNEL	RHSRRQLPPVPPKPRPLL	159	-	-	+	+	+	-	-	+	-	-	-	-	-	-
bSH3015	Nef	EKVGFPVTPQVPLRPMTY	160	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3016	MUS CADHERIN	PQPHRVLP TSPSDIA	161	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3017	AP2	ADFQPPYFP PPYQPTYPQS	162	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3018	ACTIN BINDING	SSAAPPPPPRRATPEK	163	-	+	+++	-	-	+++	-	+++	-	-	+	+++	-	-

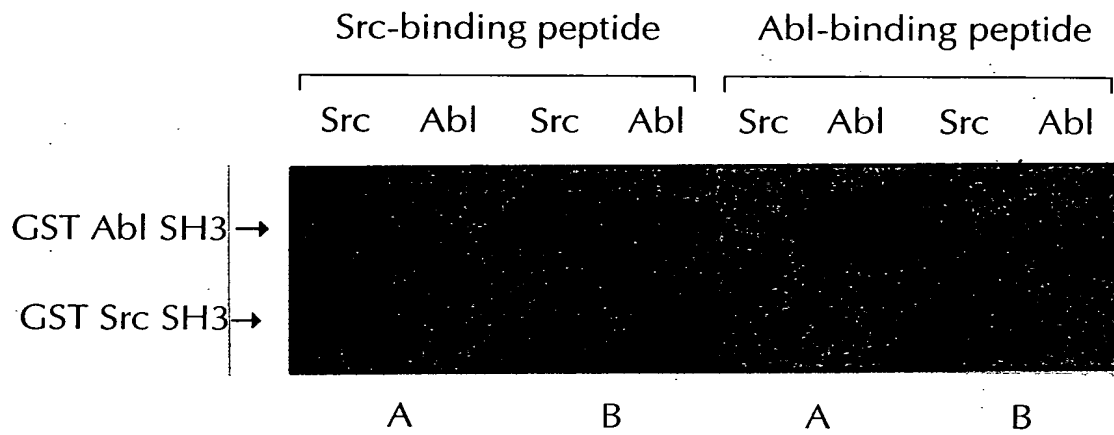
FIG.12A

FIG. 12B

SEQ. ID NO.

	NUMBER OF DOMAINS ENCODED BY CLONE	
	1 4 3 1 1 1 1 1 2 3 1 1 1 1	5

FIG. 13

**FIG. 14**

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α GST Ab

Cortactin

Abl

Src

Src

Yes

Abl

Cortactin

p53bp2

PLCy

Crk

Grb2 N

Grb2 C

Nck N

Nck M

Nck C

FIG. 15

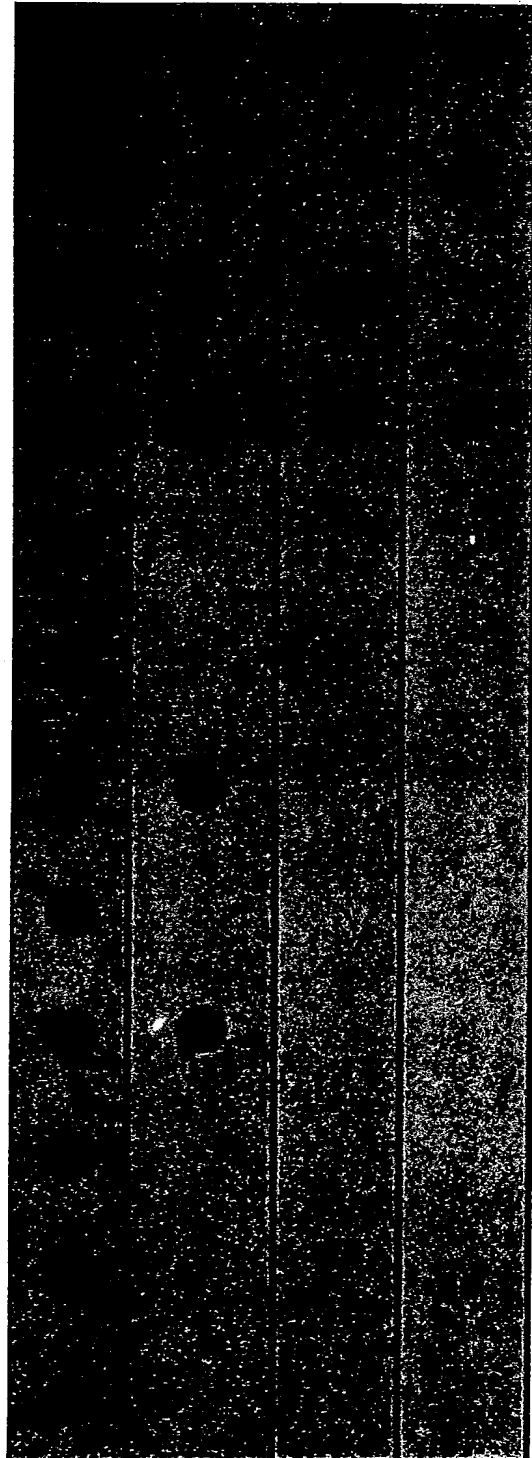
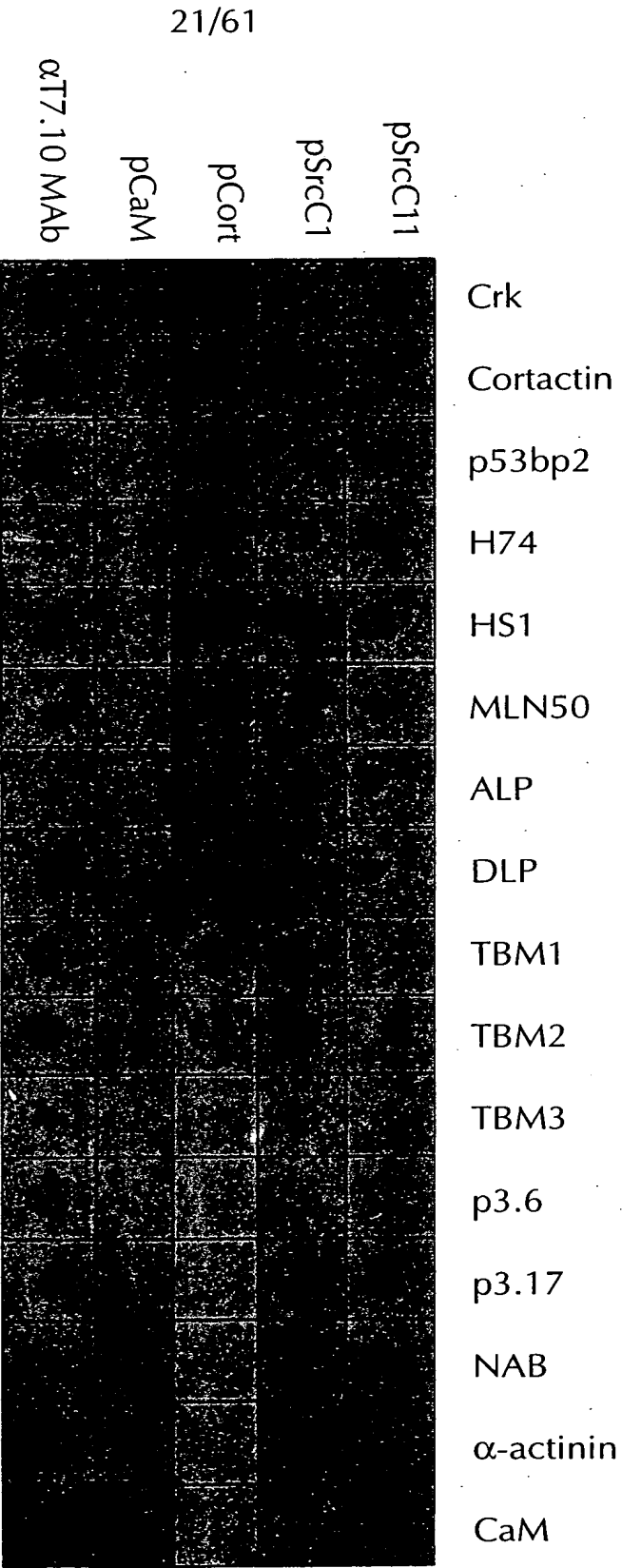


FIG. 16



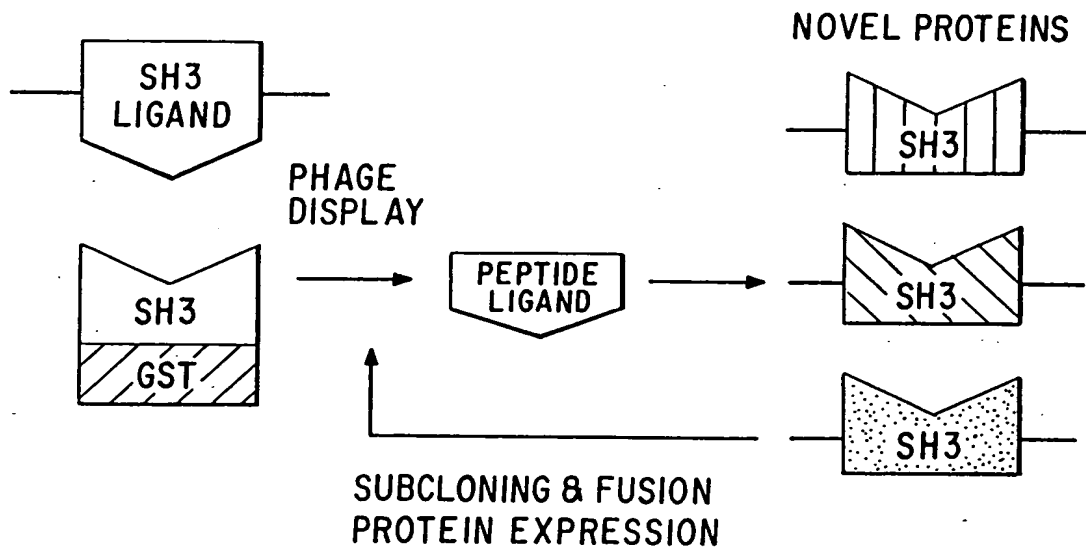


FIG. 17

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1   GTGAATGCTG CAGACAGTGA CGGATGGACA CCACTGCATT
41  GTGCTGCCTC TTGCAACAGT GTCCACCTCT GCAAGCAGCT
81  GGTGGAAAGT GGAGCCGCTA TCTTTGCCTC CACCATCAGT
121 GACATTGAGA CTGCTGCAGA CAAGTGTGAA GAGATGGAAG
161 AGGGATACAT CCAGTGTTCC CAGTTTCTGT ATGGGGTACA
201 AGAGAAGCTG GGAGTGATGA ACAAAGGCAC CGTGTATGCT
241 TTGTGGGACT ACGAGGCCCA GAACAGCGAT GAGCTGTCCT
281 TCCATGAAGG GGATGCCATC ACCATCCTGA GGCACAAAGA
321 TGA AACGAG ACCGAGTGGT GGTGGGCTCG TCTTGGGGAC
361 CGGGAGGGCT ACGTGCCCAA AAATTGCTG GGGTTGTATC
401 CACGGATCAA ACCCCGGCAG CGAACACTTG CCTGAACCCC
441 CTGGAGTACC ACAGTCTCGT TTGCTCCCAG GAGCTACTGG
481 AGGAGATCCC ACTGCCCTGG GAAACTGAA GCTAGGATGG
521 TCTCCTGGTG CTCACCTTAG CAGACAGTGT CCACAATGTG
561 AATCCCACTT CCCAGGTGAG GCCCTCTCCA GGCTGCAGGA
601 GCTGG (SEQ. ID NO:5)

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FIG. 18

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1   VNAADSDGWT PLHCAASCNS VHLCKQLVES GAAIFASTIS
41  DIETAADKCE EMEEGYIQCS QFLYGVOEKL GVMNKGTVYA
81  LWDYEAQNSD ELSFHEGDAI TILRRKDENE TEWWWARLGD
121 REGYVPKNLL GLYPRIKPRQ RTLA (SEQ ID NO:6)

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FIG. 19

```

1   SGCARSGAAA ASAGLAPSCR VRVGLPRLSL VAPCSAMSKP
41  PPKPVKPGQV KVFRLYTFE PRTPDELYFE EGDIIYITDM
81  SDTSWWKGTC KGRTGLIPSN YVAEQAESID NPLHEAAKRG
121 NLSWLRECLD NRVGVNGLDK AGSTALYWAC HGGHKDIVEV
161 LFTQPNVELN QQNKLGDAL HAAAWKGYAD IVQLLLAKGA
201 RTDLRNNEKK LALDMATNAA CASLLKKKQQ GTDGARTLSN
241 AEDYLDEDS D (SEQ ID NO:8)

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FIG 21

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1      GAATTCAA GCTCGGGTTG CGCGCGGTCC GGAGCGGCCG
41     CGGCCAGCGC AGGCTTGGCG CCCAGTTGTC GTGTGCGTGT
81     GGGGCTCCCG CGGCTGAGCC TGGTCGCTCC GTGTAGCGCC
121    ATGTCCAAGC CACCTCCCAA ACCGGTCAAA CCAGGGCAAG
161    TTAAAGTCTT CAGAGCTCTA TATACATTTG AACCCAGAAC
201    TCCAGATGAA TTATACTTTG AAGAAGGAGA CATTATCTAC
241    ATCACTGACA TGAGTGATAC CAGCTGGTGG AAAGGGACAT
281    GCAAGGGCAG AACAGGACTG ATCCCAGCA ACTATGTGGC
321    TGAGCAGGCA GAATCCATTG ACAATCCATT GCATGAAGCT
361    GCAAAAAGAG GCAACCTGAG CTGGTTGAGG GAGTGCTTGG
401    ACAACCGGGT GGGTGTGAAC GGCCTGGACA AAGCTGGAAG
441    CACAGCCCTG TACTGGGCCT GCCACGGTGG CCATAAAGAC
481    ATAGTGAGG TTCTGTTTAC TCAGCCGAAT GTGGAGCTGA
521    ACCAGCAGAA TAAGCTGGGA GACACAGCTC TGCACGCGGN
561    TGCCTGGAAG GGTATGCAAG ACATTGTCCA GTTGCTACTG
601    GCAAAAGGTG CGAGGACAGA CTTGAGAAAC AATGAGAAGA
641    AGCTGGCCTT GGACATGGCC ACCAACGCTG CCTGTGCATC
681    GCTCCTGAAG AAGAAGCAGC AGGGAACAGA TGGGGCTCGA
721    ACGTTAAGCA ACGCCGAGGA CTACCTCGAT GACGAAGACT
761    CAGACTGATT CCCCCGGGG CCGCTTTGAT TGTTGCCTAA
801    ACTTCTTTTG CTTTTGCCAT TCCGGAGCCT GGGTTGTTTG
841    CCAGAAGAGT ATTGATAACT GTTGCTTTTA AAGTCTGTAT
881    GAGCGCGACA CTGCTGCACT GTGATCTGTG AGGAGTCGTT
921    GTGAGGGTGG CTCATTCTCA CCCACGCCTT GNCAATAAGT
961    GAAGAGATAC TTTGTTGTAT AAAATACATA TATGCTCACC
1001   AGGGTAAAAT AAACGAAAAA AANTTATTTT TATTTATCAA
1041   GCTAAAAAAA AAAAGCTTGG GCCCTNTTCT ATAGTGTCAC
1081   CTAAATACTA GCTTGANCCG GNTGCTAACA AAGCCCGAAA
1121   GGAAGCTGAG TTGCTGCTGC CACCGNTGAG CAATAACTAG
1161   CATANCCCT TGGGGCCTCT AAACGGGTCT TGAGGGGTTT
1201   TTNGNTGAAA GGAGGANCTA TTTCCGGATA ACCTGGNGTA
1241   ATAGGGAAGA GGCCCGNACC GATCGCCCTT CCCAACAGA
```

(SEQ ID NO: 7)

FIG. 20


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1   .ACTCACGNC GGTGGAGTGG TACCGGATCG AATTCAAGCC GCATCACTGG
51  CACTGGACGC CAGGGCATCT TCCCTGCCAG CTACGTGCAG ATAAACCGAG
101 AGCCCCGGCT CAGGCTTTGT GATGATGGTC CCCAGCTCCC TGCATCACCT
151 AACCCGACAA CCACTGCTCA CCTAAGCAGC CACTCCCACC CCTCCTCAAT
201 ACCTGTGGAC CCCACTGACT GGGGAGGTCG AACCTCCCCT CGACGCTCCG
251 CCTTTCCCTT CCCCATCACC CTCCAGGAGC CCAGATCCCA AACCCAGAGT
301 CTCAATACCC CTGGACCAAC CCTGTCCCAT CCTCGAGCCA CCAGCCGTCC
351 CATAAACCTG GGACCCTCCT CCCCAAACAC AGAGATACAC TGGACTCCGT
401 ACCGGGCCAT GTACCAGTAC AGGCCCCAGA ATGAGGACGA GCTGGAACCT
451 CGAGAGGGGG ACCGTGTGGA TGTGATGCAG CAATGTGACG ATGGCTGGTT
501 TGTGGGTGTC TCCCGGCGAA CTCAGAAATT TGGGACATTC CCTGGAATT
551 ATGTAGCCCC AGTGTGAGTG GTCTCCATGG CAGTTTGGAG CCAACGAGGA
601 TCGGGAGGGG AGCAGTAGCA CTATGGGAGG GAGAGAGGCC TTCCATAGCC
651 TCCTCCCCAG GACCTGTGCT CCCAGCTTCT GCAGAGACCC CAGCAACTTT
701 CCCTCCAAGC CTCCTTGAAG TCCGATTCCC ACCCGCAAG TCACAGGCAT
751 TCCTTTGACA GCCCCCTTCA CCGCCCCTCA AATACAGACA TCTGCTTTCA
801 TGTGGGNAAA AAAAAAAAT TAAAAGGTGG CCCTAT (SEQ ID NO:9)

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FIG.22

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1   RITGTGRQGI FPASYVQINR EPRLRLCDDG PQLPASNPNT
41  TTAHLSSHSH PSSIPVDPTD WGGRTSPRRS AFPFPITLQE
81  PRSQTQSLNT PGPTLSHPRA TSRPINLGPS SPNTEIHWTP
121 YRAMYQYRPQ NEDELELREG DRVDVMQQCD DGWFGVGSRR
161 TQKFGTFPGN YVAPV (SEQ ID NO:10)

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FIG.23

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1   MSVAGLKKQF HKATQKVSEK VGGAEGTKLD DDFKEMERKV
41  DVTSRAVMEI MTKTIEYLQP NPASRAKLSM INTMSKIRGO
81  EKGPGYPQAE ALLAEAMLKF GRELGDDCNF GPALGEVGEA
121 MRELSEVKDS LDMEVKQNF I DPLQNLHDKD LREIQHHLKK
161 LEGRRLDIFY KKKRQGIKIPD EELRQALEKF DESKEIAESS
201 MFNLLEMDIE QVSQLSALVQ AQLEYHKQAV QILQQVTVRL
241 EERIRQASSQ PRREYQPKPR MSLEFATGDS TQPNGGLSHT
281 GTPKPPGVQM DQPCCRALYD LEPENEGELA FKEGDIITLT
321 NQIDENWYEG MLHGQSGFFP INYVEILVAL PH
      (SEQ ID NO:12)

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FIG.25

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1 TNNNNYYMM SKYSKKGKKK KGKWMSGRTC GATTCAAGCC GACCAGCGGC
51 GGCCCGGCGA CCCAGCCGC CTCTCCGCAT CTGCATCTGC ATCTGCCGGC
101 CGCGCAGCCT CCCGCATCCC ATCATGTCGG TGGCAGGGCT GAAGAAGCAG
151 TTCCACAAAG CCACTCAGAA AGTGAGTGAG AAGGTGGGAG GAGCGGAAGG
201 CACCAAGCTC GATGATGACT TCAAAGAGAT GGAGAGGAAA GTGGATGTCA
251 CCAGCAGGGC TGTGATGGAG ATAATGACAA AAACGATTGA ATACCTCCAA
301 CCCAATCCAG CTTCCAGGGC TAAGCTCAGT ATGATCAACA CCATGTGCGA
351 AATCCGCGGC CAAGAGAAGG GGCCAGGCTA CCCTCAGGCG GAAGCACTGC
401 TGGCAGAGGC CATGCTCAAG TTCGGCAGGG AGCTGGGTGA TGATTGCAAC
451 TTTGGTCCTG CTCTCGGTGA GGTGGGAGAA GCCATGAGGG AGCTCTCGGA
501 GGTCAAGGAC TCATTGGACA TGGAAGTGAA GCAGAATTTT ATCGACCCCC
551 TTCAGAATCT TCATGACAAG GATCTGAGGG AGATTGAGCA TCATCTGAAA
601 AAGCTGGAAG GCCGACGCTT AGACTTTGGT TATAAGAAGA AGCGACAAGG
651 CAAGATTCCA GATGAAGAAC TCCGCCAAGC TCTGGAGAAA TTCGATGAGT
701 CTAAAGAAAT CGCCGAGTCG AGCATGTTCA ACCTCTTGGA GATGGATATA
751 GAACAGGTGA GCCAGCTCTC CGCACTTGTT CAGGCTCAGC TGGAGTACCA
801 CAAGCAGGCA GTGCAGATCC TGCAGCAGGT CACTGTCAGA CTGGAAGAAA
851 GAATAAGACA AGCTTCATCT CAGCCAAGAA GGGAAATATCA GCCCAAACCA
901 CGGATGAGCC TAGAGTTTGC CACTGGAGAC AGTACTCAGC CCAACGGGGG
951 TCTCTCCAC ACAGGCACAC CCAAACCTCC AGGTGTCCAA ATGGATCAGC
1001 CCTGCTGCCG AGCTCTGTAT GACTTGGAAC CTGAAAATGA AGGGGAATTG
1051 GCTTTTAAAG AGGGCGATAT CATCACACTC ACTAATCAGA TTGACGAGAA
1101 CTGGTATGAG GGGATGCTTC ATGGCCAGTC TGGCTTTTTC CCCATCAACT
1151 ATGTAGAAAT TCTGGTTGCT CTGCCCCATT AGGATCCTGT GCTGGCTGGC
1201 TCACCTCCTT CTGACCCAGA TAGTTAAGTT TAACCACTGC TTTGGTAATG
1251 CTGCTTCCAA TACATCACGA ATGCAGGCCG CAGTGGATGA GTCACCAAGC
1301 CCACACGTGC CCTGGGTTGA CCCGTGTGCT CCTCCAGGAG ACGCGGTGAT
1351 AGATGGTATC TTCCAAGGCC AGTGGGCCTG GTACATGCTT TAAACACCA
1401 TCTGAGACTA GCCAGGAGTC CCAGAACTGG CTTACAGTT CTCAGGAGGC
1451 TGTGGTTCCT GGTAACATGC CTGTGAACCA CATGGCAGAA AAATCTCTCT
1501 CACTGAAGAT ATTGTCTCTC ACCCAGGGGC CATCTCAAGG TCTCCAGTTC
1551 TCCATTTACA GAGGAGAAAG TCCTTTTGTG TGCATTTTCC CTTCTAAAT
1601 ATGTGAGTCA CAGAATTGTT GGCAAAAACA TCCCCTCACC AGCAAGATGT
1651 CTGCTGGTTT AAGCAACTTG GTCTCTTGAT GCCATTAGCA AAAGTATTAA
1701 TTGTCCAAAG CACCTTTGTT CACTAATATC TATCTATCTA TCTATCTATC
1751 TATCTATCTA TCTATCTATC TATCTATCAT CTATCTACCT ACCTATCTAC
1801 CTATCATCTA TCTATCTATC ATCTATTATC TATCTATCTA TCTATCTATC
1851 NNTCNATCTA TCTATCTATC CATCTATCTA TCCATCATCT ATCTACCTAC
1901 CTATCTACTA TCCATCTATC TATCTATCCA TCATCTATCT ACCTACCTAT
1951 CTAATATCCA TCCATTTATC TATCTATCTA TCTATCTATC TATCTATCTA
2001 TCTCCCTCAT ACTTCTGAGA CATGGCCAGT TTTCTTCCCT CCCTGCTGTT
2051 AAGCACTTGG NAGATGAGGG GGGGGGTCCC ATTTNATTTT TGAGTGAGAT
2101 GGTGAGCAGG GTGTATGTTG GCTGTNNTNN GGGGGTGGCC CTA

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(SEQ ID NO:11)

FIG. 24

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1 CGGGCGCGGC GGGAGCCTGG TGGACCCTGC TTTGGCGGTA
41 ATCATTGATC ATCGCAGATG CCCTCATATC CACTTTGGAT
81 TCCTTGGATT CGGACAGACT CTGAACTGCT TTTCCAGCA
121 AAAGAGAAAG ATGTGGAAG CCTCTGCAGG CCATGCTGTG
161 TCCATCACGC AGGATGATGG AGGAGCTGAT GACTGGGAGA
201 CTGATCCTGA TTTTGTGAAT GATGTGAGTG AAAAGGAGCA
241 GAGATGGGGT GCTAAAACCG TGCAGGGATC GGGGCACCAG
281 GAACACATCA ACATTCACAA GCTTCGAGAG AATGTCTTCC
321 AAGAACACCA GACGCTCAAG GAGAAGGAGC TGGAAACGGG
361 ACCCAAGGCT TCCCACGGCT ATGGCGGGAA GTTCGGTGTG
401 GAGCAGGATA GGATGGACAG ATCAGCCGTG GGCCATGAGT
441 ACCAGTCGAA GCTTTCCAAG CACTGCTCAC AAGTGGACTC
481 GGTCCGGGGC TTCGGAGGCA AGTTCGGTGT CCAGATGGAC
521 AGGGTGGATC AGTCTGCTGT AGGCTTTGAA TACCAGGGGA
561 AGACTGAGAA GCATGCCTCC CAGAAAGACT ACTCTAGTGG
601 CTTCGGTGGC AAATACGGTG TGCAAGCTGA CCGTGTAGAC
641 AAGAGTGCCG TGGGCTTTGA CTACCAGGGC AAGACGGAGA
681 AGCATGAGTC TCAGAAAGAT TACTCCAAAG GTTTTGGTGG
721 CAAATATGGG ATTGACAAGG ACAAGGTGGA TAAAGTGCT
761 GTGGGCTTTG AGTATCAAGG CAAGACAGAG AAGCACGAAT
801 CCCAGAAAGA CTATGTAAAA GGCTTTGGAG GAAAGTTTGG
841 TGTGCAGACA GACAGACAGG ACAAGTGTGC CCTTGGCTGG
881 GACCATCAGG AGAAGCTGCA GCTGCATGAA TCCCCAAAAG
921 ACTATAAGAC TGGTTTCGGA GGCAAATTTG GTGTTCAGTC
961 CGAGAGGCAG GACTCCTCCG CTGTGGGGTT TGATTACAAG
1001 GAGAGATTGG CCAAGCACGA GCCCCAGCAA GACTATGCCA
1041 AAGGATTCGG CGGGAAGTAT GGGGTGCAGA AGGATCGGAT
1081 GGACAAGAAT GCATCCACCT TTGAAGAAGT GGTCCAGGTG
1121 CCATCTGCCT ATCAGAAGAC TGTCCCCATT GAGGCCGTAA
1161 CCAGCAAAAC CAGTAATATC CGTGCTAACT TTGAAAACCT
1201 GGCAAAGGAG AGAGAGCAGG AGGACAGGCG GAAGGCAGAA
1241 GCCGAGAGAG CTCAGCGGAT GGCCAAAGAA AGACAGGAGC
1281 AGCAGGAGGC GCGCAGGAAG CTGGAAGAGC AAGCCAGAGC
1321 CAAGAAGCAG ACGCCCCCTG CATCCCCTAG TCCTCAACCA
1361 ATTGAAGACA GACCACCCTC CAGCCCCATC TATGAGGATG
1401 CAGCTCCGTT CAAGGCCGAG CCGAGCTACC GAGGTAGCGA
1441 ACCTGAGCCT GAGTACAGCA TCGAGGCCGC AGGCATTCTT
1481 GAGGCTGGCA GCCAGCAAGG CCTGACCTAT ACATCAGAGC
1521 CCGTGACGA GACTACAGAG GCTCCTGGCC ACTATCAAGC
1561 AGAGGATGAC ACCTACGATG GGTATGAGAG TGACCTGGGC
1601 ATCACAGCCA TCGCCCTGTA TGACTIONAG GCTGCTGGCG

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FIG. 26A

1641 ATGATGAGAT CTCCTTTGAC CCTGATGACA TCATCACCAA
1681 CATAGAAATG ATTGACGATG GCTGGTGGCG TGGGGTGTGC
1721 AAGGGCAGAT ACGGGCTCTT CCCAGCCAAC TATGTGGAGC
1761 TGCGGCAGTA GGGCTGCCAC CCAGAGCCTA CCGGCACCAG
1801 CACAGGGTTC AACTACAGA GCATCTGCGT GTGTTTGAGT
1841 TGGTTTCTGC TTCCGTTTCT GTTTTG

(SEQ ID NO:13)

FIG. 26B

29/61

1 MWKASAGHAV SITQDDGGAD DWETDPDFVN DVSEKEQRWG
41 AKTVQSGSHQ EHINIHLRE NVFQEHQTLK EKELETGPKA
81 SHGYGGKFGV EQDRMDRSV GHEYQSKLSK HCSQVDSVRG
121 FGGKFGVQMD RVDQSAVGFE YQKTEKHAS QKDYSSGFGG
161 KYGVQADRVD KSAVGFDYQG KTEKHESQKD YSKGFGGKYG
201 IDKDKVDKSA VGFEYQGKTE KHESQKDYVK GFGGKFGVQT
241 DRQDKCALGW DHQEKQLLHE SQKDYKTGFG GKFGVQSERQ
281 DSSAVGFDYK ERLAKHEPQQ DYAKGFGGKY GVQKDRMDKN
321 ASTFEEVVQV PSAYQKTVPI EAVTSKTSNI RANFENLAKE
361 REQEDRRKAE AERAQMAKE RQEQEEARRK LEEQARAKKO
401 TPPASPSQP IEDRPPSSPI YEDAAPFKAE PSYRGSEPEP
441 EYSIEAAGIP EAGSQQLTY TSEPVYETTE APGHYQAEDD
481 TYDGYESDLG ITAIALYDYQ AAGDDEISFD PDDIITNIEM
521 IDDGWWRGVC KGRYGLFPAN YVELRQ (SEQ ID NO:14)

FIG. 27

1 AAGCAGTCCT TCACCATGGT GGCCGACACT CCGGAAAACC TCCGCCTCAA
51 GCAACAGAGC GAGCTGCAGA GTCAGGTGCG CTACAAGGAG GAGTTTGAGA
101 AGAATAAGGG CAAAGGTTTC AGCGTGGTGG CAGACACGCC TGAGCTGCAG
151 AGAATCAAGA AGACCCAGGA CCAGATCAGC AATATCAAAT ACCATGAGGA
201 GTTTGAGAAG AGCCGCATGG GGCCCAAGTG AGGAGAAGGG GTGGAACCCAG
251 AGCGCCGAGA AGCCCAGGAC AGCAGCAGCT ACCGGAGGCC CACAGAGCAG
301 CAGCAGCCGC AGCCTCACCA TATCCCGACC AGTGCCCCCG TGTACCAGCA
351 GCCCCAGCAG CAGCAGATGA CCTCGTCCTA TGGTGGGTAC AAGGAGCCAG
401 CAGCCCCTGT CTCCATACAG CGCAGTGCCC CAGGTGGCGG TGGGAAACGG
451 TACCGTGCAG TGTATGACTA CAGCGCTGCC GACGAGGACG AGGTCTCCTT
501 CCAGGATGGG GACACCATCG TCAATGTGCA GCAGATCGAT GACGGCTGGA
551 TGTACGGGAC CGTAGAGCGC ACCGGTGACA CGGGGATGCT GCCAGCCAAC
601 TACGTGGAGG CCATCTGAAC CCTGTGCCGC CCCGCCCTGT CTTCAATGCA
651 TTCCATGGCA TCACATCTGT CCTGGGGCCT GACCCGTCCA CCCTTCAGTG
701 TCTCTGTCTT TTAAGATCTT CAACTGCTTC TTTATCCCCG CCCCTCCAGC
751 TTATTTTACC ATCCCAAGCC TTGTTCTGCC CCTGTCATGG GCTCCTTCCT
801 CTGGCAGGTT TTCCCTTGGA CCAATCAACT GATTGATTTT TCTCTCTGGA
851 TGGAACAGGC TGGGCACTCT GGGGAGGGCA GGATTGTTCT TAGCTAGGTA
901 GACTCCCAGG GCTGGGCTGA ACTAGGAGAC CCACTAAGGA GATCAGTTTA
951 GACTGGGTGC AGTGGAAC AACCTTAATT CCCAGCGAAG GGAGTCAGAG
1001 GCAGGCAGAT CTGTGACTTG GAAGCCAGCC TGGTCTACAT CGAGAGTTTC
1051 AGGACAGCCA GAGCTATGTA GTGAGGCCCT GTCTCGGAGG AAGAGTGGGG
1101 GTTGGTTAGC TCTCAGCTTC ACTTCCTGCC TTAGGCTCCT CAGAACCCCT
1151 GGCCCAAGCTC CCCCAACTCC CTTCTCCTA GAGGTGGGGT GAGCTGTGC
(SEQ ID NO:15)

FIG. 28

1 KQSFTMVADT PENLRLKQQS ELQSQVRYKE EFEKNKGKGF SVVADTPELQ
 51 RIKKTQDQIS NIKYHEEF EK SRMGPSGGEG VEPERREAQD SSSYRRPTEQ
 101 QQPQPHHIPT SAPVYQQPQQ QQMTSSYGGY KEPAAPVSIQ RSAPGGGGKR
 151 YRAVYDYSAA DEDEVSFQDG DTIVNVQQID DGWMYGTVER TGD TGMLPAN
 201 YVEAI (SEQ ID NO:16)

FIG. 29

1 ATGGCGGTGA ACCTGAGCCG GAACGGGCCG GCGCTGCAGG AGGCCTACGT
 51 GCGCGTAGTC ACCGAGAAAT CCCCAGCCGA CTGGGCTCTT TTTACCTATG
 101 AAGGCAACAG CAATGACATC CGTGTGGCTG GCACAGGAGA GGGAGGCCTG
 151 GAGGAGCTGG TGAAGAGCT CAACAGCGGG AAGGTGATGT ACGCCTTCTG
 201 CAGGGTGAAG GACCCCACT CCGGCCTGCC CAAGTTTGTC CTCATCAACT
 251 GGACAGGAGA GGGTGTGAAT GATGTGCGGA AAGGAGCATG TGCCAACCAC
 301 GTCAGCACCA TGGCCAATT CCTGAAGGGT GCCCAGTGA CCATCAATGC
 351 CCGGGCCGAG GAGGATGTGG AGCCTGAGTG CATCATGGAG AAGGTTGCCA
 401 AGGCCTCTGG GGCCAAC TAC AGCTTCCATA AGGAAAGCAC CTCCTTCCAG
 451 GATGTAGGGC CGCAGGCCCC AGTGGGCTCT GTGTACCAGA AGACCAATGC
 501 CATATCTGAG ATCAAGAGAG TCGGCAAGGA TAACTTCTGG GCCAAAGCTG
 551 AGAAGGAAGA AGAGAACCGC CGCCTGGAGG AGAAGCGGCG TGCCGAAGAG
 601 GAGCGGCAGC GGTGAGGGA GGAGCGACGA GAGCGGGAGC TGCAGGAGGC
 651 TGCCCGACGT GAGCAGCGCT ACCAGGAACA GCACAGATCA GCTGGAGCCC
 701 CGAGCAGGAC AGGTGAGCCA GAGCAGGAAG CCGTTTCAAG GACCAGACAG
 751 GAGTGGGAGT CTGCTGGGCA GCAGGCCCA CACCCACGAG AGATTTTCAA
 801 GCAGAAGGAA AGGGCAATGT CCACCACCTC TGTCACCAGC TGCAGCCGG
 851 GCAAGCTGAG GAGCCCCTTC CTGCAGAAGC AACTCACTCA ACCAGAAACC
 901 TCCTACGGCC GAGAGCCAC AGCTCCTGTC TCCCGGCTG CAGCAGGTGT
 951 CTGTGAGGAG CCAGCGCCTA GCACTCTGTC TTCTGCCAG ACAGAAGAAG
 1001 AACCTACATA TGAAGTACCC CCAGAGCAGG ACACCCTCTA TGAGGAACCA
 1051 CCACTGGTAC AGCAGCAAGG GGCTGGCTCC GAACACATTG ACAACTACAT
 1101 GCAGAGCCAG GGCTTCAGTG GACAAGGGCT GTGCGCCCGG GCCTTGATG
 1151 ACTACCAGGC AGCTGATGAC ACCGAGATCT CCTTTGACCC TGAGAACCTA
 1201 ATCACAGGCA TCGAGGTGAT TGACGAAGGC TGGTGGCGAG GCTATGGGCC
 1251 TGACGGCCAC TTTGGCATGT TTCCTGCCAA CTACGTGGAG CTCATAGAGT
 1301 GA (SEQ ID NO:17)

FIG. 30

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1  MAVNLSRNGP ALQEAYVRVV TEKSPTDWAL FTYEGNSNDI RVAGTGEGGL
51  EELVEELNSG KVMYAFCRVK DPNSGLPKFV LINWTGEGVN DVRKGACANH
101 VSTMANFLKG AHVTINARAE EDVEPECIME KVAKASGANY SFHKESTSFO
151 DVGPOAPVGS VYQKTNAISE IKRVGKDNFW AKAEKEEENR RLEEKRRAAE
201 ERORLEEERR ERELQEAARR EORYQEQRHS AGAPSRTGEP EQEAVSRTRQ
251 EWESAGQQAP HPREIFKQKE RAMSTTSVTS SQPGKLRSPF LQKQLTQPET
301 SYGREPTAPV SRPAAGVCEE PAPSTLSSAQ TEEPTYEVP PEQDTLYEEP
351 PLVQQQGAGS EHIDNYMQSQ GFSGQGLCAR ALYDYQAADD TEISFDPENL
401 ITGIEVIDEG WWRGYGPDGH FGMFPANYVE LIE (SEQ ID NO:18)

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FIG. 31

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1  MSVAGLKKQF YKASQLVSEK VGGAEGTKLD DDFKDMEKKV DVTSKAVAEV
51  LVRTIEYLQP NPASRAKLTN LNTVSKIRGQ VKNPGYPQSE GLLGECMVRH
101 GKELGGESNF GDALLDAGES MKRLAEVKDS LDIEVKQNF I DPLQNLCDKD
151 LKIEQHHLKK LEGRRLDFDY KKKRQGKIPD EELRQALEKF EESKEVAETS
201 MHNLLTDIE QVSQLSALVD AQLDYHRQAV QILEELADKL KRRVREASSR
251 PKREFKPRPR EPFELGELEQ PNGGFPCAPA PKITASSSFR SSDKPIRMPS
301 KSMPLDQPS CKALYDFEPE NDELGFGFREG DLITLTNQID ENWYEGMLHG
351 QSGFFPLSYV QVLVPLPQ (SEQ ID NO:20)

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FIG.33

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1  MAEMGSKGVT AGKIASNVQK KLTRAQEKVL QKLGKADETK DEQFEQCVQN
51  FNKQLTEGTR LQKDLRTYLA SVKAMHEASK KLSECLQEVY EPEWPGRDEA
101 NKIAENNDLL WMDYHQKLVD QALLTMDTYL GQFPDIKSRI AKRGRKLVQY
151 DSARHHYESL QTAKKKDEAK IAKAEELIK AOKVFEEMNV DLQEELPSLV
201 NSRVGFYVNT FQSIAGLEEN FHKEMSKLNQ NLNDVLVSLE KQHGSNTFTV
251 KAQPSDNAPE KGNKSPSPPP DGSPAATPEI RVNHEPEPAS GASPGATIPK
301 SPSQPAEASE VVGGAQEPGE TAASEATSSS LPAVVVETFS ATVNGAVEGS
351 AGTGRDLPP GFMFKVQAQH DYTATDDEL QLKAGDVVLV IPFONPEEQD
401 EGWLMGVKES DWNQHKLEK CRGVFPENFT ERVQ (SEQ ID NO:22)

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FIG. 35

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1  TTNNCACTCA CCGTCCGTGG TNNNNSTMMC SGWYNKRNTK YRRKMSSKRW
51  YKWKKCRRKS GCGGCGCCGA CCTGCGCGCG GAGGAAAGAA GTCGGTTCGG
101 CGGCGCCGGC GGAAACCGGA GTTCGAGCGG GAGGCCTGAC GCGGCAGGC
151 GGCATGTCGG TGGCGGGGCT GAAGAAGCAG TTCTACAAGG CGAGCCAGCT
201 GGTCAAGCAG AAGGTTGGTG GGGCCGAAGG GACCAAACTG GATGATGACT
251 TTAAAGATAT GAAAAAGAAG GTGGATGTCA CCAGCAAGGC CGTGGCAGAG
301 GTGCTGGTCA GAACCATAGA ATATCTGCAG CCTAACCCAG CCTCGAGAGC
351 CAAGCTGACT ATGCTGAACA CCGTATCCAA GATCCGGGGC CAAGTGAAGA
401 ACCCTGGCTA CCCACAGTCA GAGGGTCTGT TGGGAGAGTG CATGGTTCGC
451 CATGGCAAGG AACTAGGTGG AGAGTCCAAC TTCGGTGATG CCCTGCTAGA
501 TGCAGGTGAG TCCATGAAGC GCCTGGCTGA GGTGAAGGAC TACTGGACA
551 TCGAGGTCAA GCAGAACTTC ATTGACCCAC TACAGAACCT GTGTGACAAG
601 GATCTGAAGG AGATCCAGCA CCACCTGAAG AAATTGGAGG GCCGCCGCCT
651 TGACTTTGAC TACAAGAAGA AGCGCCAGGG CAAGATCCCC GATGAGGAGC
701 TGCGCCAGGC CCTAGAGAAG TTCGAGGAGT CCAAGGAGGT GCGGGAGACC
751 AGTATGCACA ACCTCCTGGA GACTGATATA GAGCAGGTGA GCCAGCTCTC
801 GGCCCTGGTG GATGCCCAGC TGGACTACCA CCGGCAGGCA GTGCAGATCC
851 TGGAGGAGCT GGCTGACAAG CTGAAGCGCA GGGTTCGGGA AGCCTCCTCA
901 CGCCCCAAGC GGGAGTTCAA GCCCCGGCCC CGGGAGCCCT TTGAGCTTGG
951 AGAGCTGGAG CAGCCCAATG GGGGATTCCC CTGTGCCCCA GCACCTAAGA
1001 TCACAGCCTC CTCATCATTT AGATCGTCAG ACAAGCCCAT CAGGATGCCC
1051 AGCAAGAGCA TGCCACCCCT GGACCAGCCA AGCTGCAAGG CGCTTTATGA
1101 TTTTGAGCCA GAGAATGATG GCGAGCTGGG CTTCCGTGAG GGGGACCTCA
1151 TCACGCTTAC CAACCAGATC GACGAGAACT GGTATGAGGG GATGCTGCAC
1201 GGCCAATCAG GCTTCTTCCC ACTCAGCTAC GTGCAGGTGC TGGTGCCTCT
1251 GCCTCAGTGA CTGGGCCTTT ACACCGCTGC CAGTCACAGT GCAGCAGCAG
1301 TCTAATGCCA AGGTGCTCTA GAAACACTAA TGTTCTCTCA GGGGGGACTC
1351 CTCCCCACTC CCTCAGCCCT GGGGCCCCC TATCCTAAGA CTCGGAAAGG
1401 CCCACCCTGA GGTTCTATTG CCTTCCTGGT GGTATCAGCT TCCAGCTGTT
1451 TCAACCCTTC CCAGCCCGTT GCTGGCGATG GSCNNYGCC CCCTCTCTAG
1501 GCTCTCTAGA GGCAGGCAGG TCCTTGGAAT CCCAGCCTG CAAGCAGAGG
1551 CTGGCCAGCT CCCAGCTCA GCACACAGAC ACACCTGGCA CCTGCTGCTC
1601 ATGAAGAAGT GCACAAGGCA CAAATGTGTA CACTTCCCAT GGGACCACAG
1651 ACCCAGCTCA GCTCTGTTGA AGACCAAGCA CAAAGGCCTT GAAGAGTGGA
1701 CATTCCCAGG TCCCTGGCAC CTTCCCTTGA GCCAGCTCCA TTGCTACTTA
1751 TTCATGTGAC TGAAGCTGAC CACAGGCAGC TGGCAGGTCC TTTTTTCAAC
1801 CAGCAGGCTA GGCTGGCCAT AGACCCAGCT CTGCCTCACC CTGCCATGTT
1851 CCAGTAATGG AGGCCTCCAG CCTGGGCTCT ATTACATTCT TCTCTACAGC
1901 TGCCCCATAA CCCGTGGCTT ATCCCTGGCA CGTGGGGCCA CACCCACGCG
1951 CCCCTGGATA GGCAACACTG TCCTGCTCCA GCCTGTGCTG ANATGAAGTG
2001 TACTCCTAAT TTTTTTTTAA AAAAAAAGTA TTAAATNTCT CTTTCTATAT
2051 AAAANAAAGN TGGCCCTANN NGGA (SEQ ID NO:19)

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FIG. 32


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1 CCTCACTCGC TCTCCCCGCG CACGCTCCGT CTCCGTCAGT CCCCTGAGCT
51 GTTCTAGTGC GCGGCGTGGA GCCAGGGCTC AGGCTGGTGG AGCGGCCGGG
101 GCTGGAGGCT GGGAGTGCGG CGCGCACGGC CTCCCCGCGC CATTATCCGC
151 GCTCGCTTCG GGCAGAGCCG GCGCCAGGAT GGCAGAGATG GGGAGCAAGG
201 GGGTGACGGC GGGGAAGATC GCCAGCAACG TACAGAAGAA GCTGACCCGA
251 GCGCAGGAGA AGGTCCTGCA GAAACTGGGG AAGGCGGACG AGACGAAGGA
301 CGAGCAGTTT GAGCAGTGTG TCCAGAACTT CAATAAGCAG CTGACAGAGG
351 GTACCCGGCT GCAGAAGGAT CTTCGGACCT ATCTGGCTTC TGTAAAGCG
401 ATGCACGAAG CCTCCAAGAA GCTGAGTGAG TGTCTTCAGG AGGTGTACGA
451 GCCCGAGTGG CCTGGCAGGG ATGAAGCAAA CAAGATTGCA GAGAACAATG
501 ACCTACTCTG GATGGACTAC CACCAGAAGC TGGTGGACCA GGCTCTGCTG
551 ACCATGGACA CCTACCTAGG CCAGTTCCTT GATATCAAGT CGCGCATTGC
601 CAAGCGGGGG CGGAAGCTGG TGGACTATGA CAGTGCCCGG CACCACTATG
651 AGTCTCTTCA AACCGCCAAA AAGAAGGATG AAGCCAAAAT TGCCAAGGCA
701 GAAGAGGAGC TCATCAAAGC CCAGAAGGTG TTCGAGGAGA TGAACGTGGA
751 TCTGCAGGAG GAGCTGCCAT CCCTGTGGAA CAGCCGTGTA GGTTTCTATG
801 TCAACACGTT CCAGAGCATC GCGGGTCTGG AGGAAAACTT CCATAAAGAG
851 ATGAGTAAGC TCAATCAGAA CCTCAATGAT GTCCTGGTCA GCCTAGAGAA
901 GCAGCACGGG AGCAACACCT TCACAGTCAA GGCCCAACCC AGTGACAATG
951 CCCCTGAGAA AGGGAACAAG AGCCCGTCAC CTCCTCCAGA TGGCTCCCCT
1001 GCTGCTACCC CTGAGATCAG AGTGAACCAT GAGCCAGAGC CGGCCAGTGG
1051 GGCCTCACCC GGGGCTACCA TCCCAAGTC CCCATCTCAG CCAGCAGAGG
1101 CCTCCGAGGT GGTGGGTGGA GCCCAGGAGC CAGGGGAGAC AGCAGCCAGT
1151 GAAGCAACCT CCAGCTCTCT TCCGGCTGTG GTGGTGGAGA CCTTCTCCGC
1201 AACTGTGAAT GGGGCGGTGG AGGGCAGCGC TGGGACTGGA CGCTTGGACC
1251 TGCCCCCGGG ATTCATGTTT AAGGTTCAAG CCCAGCATGA TTACACGGCC
1301 ACTGACTG ATGAGCTGCA ACTCAAAGCT GGCGATGTGG TGTGGTGAT
1351 TCCTTTCCAG AACCCAGAGG AGCAGGATGA AGGCTGGCTC ATGGGTGTGA
1401 AGGAGAGCGA CTGGAATCAG CACAAGGAAC TGGAGAAATG CCGCGGCGTC
1451 TTCCCGGAGA ATTTTACAGA GCGGCTACAG TGACGGAGGA GCCTTCCGGA
1501 GTGTGAAGAA CCTTTCCCCC AAAGATGTGT G (SEQ ID NO:21)

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FIG. 34

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1 GAATTCGTCG ACCCACGCGT CCGGTTTGAG CAGTGCGTCC
41 AGAATTTCAA CAAGCAGCTG ACGGAGGGCA CCCGGCTGCA
81 GAAGGATCTC CGGACCTACC TGGCCTCCGT CAAAGCCATG
121 CACGAGGCTT CCAAGAAGCT GAATGAGTGT CTGCAGGAGG
161 TGTATGAGCC CGATTGGCCC GGCAGGGATG AGGCAAACAA
201 GATCGCAGAG AACAAACGACC TGCTGTGGAT GGATTACCAC
241 CAGAAGCTGG TGGACCAGGC GCTGCTGACC ATGGACACGT
281 ACCTGGGCCA GTTCCCCGAC ATCAAGTCAC GCATTGCCAA
321 GCGGGGGCGC AAGCTGGTGG ACTACGACAG TGCCCCGCAC
361 CACTACGAGT CCCTTCAAAC TGCCAAAAAG AAGGATGAAG
401 CCAAAATTGC CAAGGCCGAG GAGGAGCTCA TCAAAGCCCA
441 GAAGGTGTTT GAGGAGATGA ATGTGGATCT GCAGGAGGAG
481 CTGCCGTCCC TGTGGAACAG CCGCGTAGGT TTCTACGTCA
521 ACACGTTCCA GAGCATCGCG GGCTGGAGG AAAACTTCCA
561 CAAGGAGATG AGCAAGCTCA ACCAGAACCT CAATGATGTG
601 CTGGTCGGCC TGGAGAAGCA ACACGGGAGC AACACCTCCA
641 CGGTCAAGGC CCAGCCCAGT GACAACGCGC CTGCAAAAGG
681 GAACAAGAGC CCTTCGCCTC CAGATGGCTC CCCTGCCGCC
721 ACCCCCGAGA TCAGAGTCAA CCACGAGCCA GAGCCGGCCG
761 GCGGGGCCAC GCCCGGGGCC ACCCTCCCCA AGTCCCCATC
801 TCAGCCAGCA GAGGCCTCGG AGGTGGCGGG TGGGACCCAA
841 CCTGCGGCTG GAGCCCAGGA GCCAGGGGAG ACGGCGGCAA
881 GTGAAGCAGC CTCCAGCTCT CTTCTGCTG TCGTGGTGGA
921 GACCTTCCA GCAACTGTGA ATGGCACCGT GGAGGGCGGC
961 AGTGGGGCCG GCGCTTGGA CCTGCCCCCA GGTTTCATGT
1001 TCAAGGTACA GGCCCAGCAC GACTACACGG CCACTGACAC
1041 AGACGAGCTG CAGCTCAAGG CTGGTGATGT GGTGCTGGTG
1081 ATCCCTTCC AGAACCCTGA AGAGCAGGAT GAAGGCTGGC
1121 TCATGGGCGT GAAGGAGAGC GACTGGAACC AGCACAAGGA
1161 GCTGGAGAAG TGCCGTGGCG TCTTCCCCGA GAACTTCACT
1201 GAGAGGGTCC CATGACGGCG GGGCCCAGGC AGCCTCCGGG
1241 CGTGTGAAGA ACACCTCCTC CCGAAAAATG TGTGGTTCTT
1281 TTTTTTGTTT TGTTTTCGTT TTTCATCTTT TGAAGAGCAA
1321 AGGGAAATCA AGAGGAGACC CCCAGGCAGA GGGGCGTTCT
1361 CCCAAAGATT AGGTCGTTTT CCAAAGAGCC GCGTCCCGGC
1401 AAGTCCGGCG GAATTCACCA GTGTCCTGAA GCTGCTGTGT
1441 CCTCTAGTTG AGTTCTGGCG CCCCTGCCTG TGCCCGCATG
1481 TGTGCCTGGC CGCAGGGCGG GGCTGGGGGC TGCCGAGCCA
1521 CCATGCTTGC CTGAAGCTTC GGCCGCGCCA CCCGGGCAAG
1561 GGTCTCTTT TCCTGGCAGC TGCTGTGGGT GGGGCCAGA
1601 CACCAGCCTA ACCTGGCTCT GCCCCGAGA CGGTCTGTGT
1641 GCTGTTTGAA AATAAATCTT AGTGTTCAAA ACAAATGAA
1681 AAAAAAAAAA TGATAAAAAA AAAAAAAAAA AAAAAAAAAA
1721 AAAAGGGCGG CCGC (SEQ ID NO: 23)

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FIG. 36

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1 EFVDPRVRFE QCVQNFNKQL TEGTRLQKDL RTYLASVKAM
41 HEASKKLNEC LQEVYEPDWP GRDEANKIAE NNDLLWMDYH
81 QKLVDQALLT MDTYLGQFPD IKSRIAKRGR KLVDYDSARH
121 HYESLOTAKK KDEAKIAKAE EELIKAQKVF EEMNVDLQEE
161 LPSLWNSRVG FYVNTFQSIA GLEENFHKEM SKLNQNLNDV
201 LVGLEKQHGS NTSTVKAQPS DNAPAKGNKS PSPPDGSPAA
241 TPEIRVNHEP EPAGGATPGA TLPKSPSQA EASEVAGGTQ
281 PAAGAEQEPGE TAASEAASSS LPAVVVETFP ATVNGTVEGG
321 SGAGRLDLPP GFMFKVQAQH DYTATDTDEL QLKAGDVVLV
361 IPFQNPEEQD EGWLMGVKES DWNQHKLEK CRGVFPENFT
401 ERVP (SEQ ID NO:24)

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FIG. 37

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1 MWKSVVGHV SVSVETQGDD WDTDPDFVND ISEKEQRWGA KTIEGSGRTE
51 HINIHQLRNK VSEEHILKK KELESGPKAS HGYGGQFGVE RDRMDKSAVG
101 HEYVADVEKH SSQTDAAARGF GGKYGVERDR ADKSAVGFDY KGEVEKHASQ
151 KDYSHGFGGR YGVEKDKRDK AALGYDYKGE TEKHESQRDY AKGFGGQYGI
201 QKDRVDKSAV GFNEMEAPTT AYKKTTPIEA ASSGARGLKA KFESLAEERK
251 KREEEKAQQ MARQQQERKA VVKMSREVQQ PSMPVEEPAA PAQLPKKISS
301 EVWPPAESHL PPESQPVRSR REYPVPSLPT RQSPLGNHLE DNEEPPALPP
351 RTPEGLQVVE EPVYEAAPEL EPEPEPDYEP EPETEPDYED VGELDRQDED
401 AEGDYEDVLE PEDTPSLSYQ AGPSAGAGGA GISAIALYDY QGEGSDELSF
451 DPDDIITDIE MVDEGWWRGQ CRGHFGLFPA NYVKLL (SEQ ID NO:26)

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FIG. 39

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1 MAGNFDSEER SSWYWGRLSR QEAVALLQGQ RHGVFLVRDS STSPGDYVLS
51 VSENSRVSHY IINSSGPRPP VPPSPAQPPP GVSPSRLRIG DQEFDSLPAI
101 LEFYKIHLYD TTTLIEPVAR SRQSGVILR QEAEYVRAL FDFNGNDEED
151 LPFKKGDILR IRDKPEEQWW NAEDSEGKRG MIPVPYVEKY RPASASVSAL
201 IGGNQEGSHP QPLGGPEPGP YAQPSVNTPL PNLONGPIYA RVIQKRPVNA
251 YDKTALALEV GELVKVTKIN VSGQWEGECN GKRGHFPFTH VRLLDQQNPD
301 EDFS (SEQ ID NO:28)

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FIG. 41

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1 CAGCCGCTGG AGGGGGCGCC TGGTGTAGAT GTGAAAAGCC GTAACCAGGA
51 ACCAGTAAAG ATGTGGAAGT CTGTAGTGGG GCATGATGTA TCGGTTTCCG
101 TGGAGACCCA GGGTGATGAC TGGGATACAG ACCCTGACTT TGTGAATGAC
151 ATCTCCGAGA AGGAGCAACG GTGGGGAGCC AAGACCATTG AGGGCTCTGG
201 ACGCACAGAG CACATCAACA TCCACCAGCT GAGGAACAAA GTGTCAGAGG
251 AGCACGACAT CCTCAAGAAG AAGGAGCTGG AATCGGGGCC TAAGGCATCC
301 CATGGCTATG GCGGTCAGTT TGGAGTGGAG AGAGACCGGA TGGACAAGAG
351 TGCCGTGGGC CACGAGTATG TTGCTGATGT GGAGAAACAC TCATCTCAGA
401 CTGATGCSGC CAGAGGCTTT GGGGGCAAAT ATGGAGTTGA GAGGGACCGG
451 GCAGACAAGT CAGCGGTGGG CTTTGACTAC AAAGGAGAAG TGGAAAAGCA
501 TGCATCTCAG AAAGATTACT CTCATGGCTT TGGTGGCCGC TACGGGGTAG
551 AGAAGGATAA ACGGGACAAA GCAGCCCTGG GATACGACTA CAAAGGAGAG
601 ACGGAGAAGC ACGAGTCTCA GAGAGATTAT GCCAAGGGCT TTGGTGGCCA
651 ATATGGAATC CAGAAAGACC GAGTGGATAA GAGTGCTGTT GGCTTCAATG
701 AAATGGAGGC CCAACCACG GCGTATAAGA AGACAACACC CATAGAAGCT
751 GCTTCCAGTG GTGCCCCTGG GCTGAAGGCA AAATTTGAGT CCCTGGCTGA
801 GGAGAAGAGG AAGCGAGAGG AAGAAGAGAA GGCACAGCAG ATGGCCAGGC
851 AGCAACAGGA GCGAAAGGCT GTGGTAAAGA TGAGCCGAGA AGTCCAGCAG
901 CCATCCATGC CTGTGGAAGA GCCAGCGGCA CCAGCCCAGT TGCCCAAGAA
951 GATCTCCTCA GAGGTCTGGC CTCCAGCAGA GAGTCACCTA CCGCCAGAGT
1001 CTCAGCCAGT GAGAAGCAGA AGGGAATACC CTGTGCCCTC TCTGCCACG
1051 AGGCAGTCTC CATTGCAGAA TCACTTGAG GACAACGAGG AGCCCCCAGC
1101 TCTGCCCCCT AGGACCCCAG AAGGCCTCCA GGTGGTGGAA GAGCCAGTGT
1151 ACGAAGCAGC ACCCGAGCTG GAGCCGGAGC CAGAGCCTGA CTATGAGCCA
1201 GAGCCAGAGA CAGAGCCTGA CTATGAGGAT GTTGGGGAGT TAGATCGGCA
1251 GGATGAGGAT GCAGAGGGAG ACTATGAGGA TGTGCTGGAG CCCGANGACA
1301 CCCCTTCTCT GTCCTACCAA GCTGGACCCT CAGCTGGGGC TGGTGGTGCG
1351 GGGATCTCTG CTATAGCCCT GTATGATTAC CAAGGAGAGG GAAGCGATGA
1401 GCTTTCCTTT GATCCAGATG ACATCATCAC TGACATTGAG ATGGTGGATG
1451 AAGGCTGGTG GCGGGGCCAA TGCCGTGGCC ACTTTGGA CTCTTCCCTGCA
1501 AACTATGTCA AGCTCCTCTA ATGACCAGCC CATTGTCTTC CGACTTCCCG
1551 AATTCGAAGC TGCTCTGCCT CCCTCTTCCC ACTCCATGGT ACTGCTGCAA
1601 GGACCTGGCT GAACATCATG AGATGCCTGA AGTTCTGGCA GTCTGTCTCC
1651 CGCCTCTTTA AGAGCTTTAG GTAGAATCGC TCCAGGTGGG GGTGGGGGTG
1701 GGGGTGGGAT CCCTCTGTCC CTCTGTGACC ACTCTTCCCT GAGGTAGCTC
1751 ATGAAATCAT CTTGCAGACC TGCCTCCTTC AGCCGCACCC CAGCTCTGCC
1801 AACCTTGCTC TAGAGTGCTG GGATTCCCTT GCCCCGACCC TGGGTGCCAG
1851 CCTAGAGGGG AGGCTCTCAC AGGGCTGCCT GATTGCCCCT GTTGTGCTTT
1901 TGCTCATTTT TCTTCCCTTA GCAGACAAAT TGGAAGTACC CTTCTGTTTA
1950 GTCCTAAAC TGAAAATAAA ATGAGACTGT GGCTAAAAA AAAAAAAAAA
2003 AAA (SEQ ID NO: 25)

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FIG. 38

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1   GGATCCCCGG AGCCGGTCCG CTGGGCGGGG CGCAGGGCTG GAGGGGCGCG
51  CGTGCCGGCG GCGGCCAGC GTGAAAGCGC GGAGGCGGCC ATGGCGGGCA
101 ACTTCGACTC GGAGGAGCGG AGTAGCTGGT ACTGGGGCCG CCTGAGCCGG
151 CAGGAGGCGG TGGCGCTATT GCAGGGCCAG CGGCACGGGG TGTTCTGGT
201 GCGGGACTCG AGCACCAGCC CCGGGGACTA TGTGCTTAGC GTCTCCGAAA
251 ACTCGCGCGT CTCCCCTAC ATCATCAACA GCAGCGGCCG GCGCCCTCCA
301 GTGCCTCCGT CGCCCGCTCA GCCTCCGCCG GGAGTGAGTC CCTCCAGGCT
351 CCGAATAGGA GATCAAGAAT TTGATTCATT GCCTGCTTTA CTGGAATTCT
401 AAAAAATACA CTATTTGGAC ACTACAACAT TGATAGAACC AGTGGCCAGA
451 TCAAGGCAGG GTAGTGGAGT GATTCTCAGG CAGGAGGAGG CAGAGTATGT
501 GCGGGCCCTG TTTGACTTTA ATGGGAATGA TGAAGAAGAT CTTCCCTTTA
551 AGAAAGGAGA CATCTGAGA ATCCGGGATA AGCCTGAAGA CGAGTGGTGG
601 AATGCAGAGG ACAGCGAAGG AAAGAGGGGG ATGATTCCTG TCCCTTACGT
651 GGAGAAGTAT AGACCTGCCT CCGCCTCAGT ATCGGCTCTG ATTGGAGGTA
701 ACCAGGAGGG TTCCCAACCA CAGCCACTGG GTGGGCCGGA GCCTGGGCCC
751 TATGCCCAAC CCAGCGTCAA CACTCCGCTC CCTAACCTCC AGAATGGGCC
801 CATTTATGCC AGGGTTATCC AGAAGCGAGT CCCTAATGCC TACGACAAGA
851 CAGCCTTGGC TTTGGAGGTC GGTGAGCTGG TAAAGGTTAC GAAGATTAAT
901 GTGAGTGGTC AGTGGGAAGG GGAGTGTAAT GGCAAACGAG GTCACCTCCC
951 ATTCACACAT GTCCGTCTGC TGGATCAACA GAATCCCGAT GAGGACTTCA
1001 GCTGAGTATA GCTCGACAGT TTGCTGACAG ATGGAACAAT CTGTTTTCCC
1051 CCAATTGCCA TCTATACAAT TTTCTTACAG GTGTCAAAGC AGTCTAGTTT
1101 ATATAAGCAT TCTGTTACCT GGGATCTTTT TTAAGACTGA ACTACTCCAT
1151 TCTCACTTGT ATTTACCATA TTCAGGTAC GAAACCGGAG GGCTTATGTG
1201 GTTAACTTCT GAGTTGGCAG TTTTAGGTGG TAGTGGCCGT GCCTGTATGA
1251 GAAGACGTAA ATACATTGCC TCCTTTCTTT TGGGCAAAC AGATCA

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(SEQ ID NO: 27)

FIG. 40

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1   MSSECDVGSS KAVVNLASG NHGPKDMDP TKICTGKGTV TLRASSSYRG
51  TPSSSPVSPQ ESPKHESKD EWKLSSADT NGNAQPSPLA AKGYRSVHPS
101 LSADKPQGS LLNEVSSSHI ETDSQDFPPT SRPSSAYPST TIVNPTIVLL
151 QHNREQQKRL SSLSDPASE RAGEQDPVPT PAELTSPGRA SERRAKDASR
201 RVVRS AQDLS DVSTDEVGIP LRNTERSKDW YKTMFKQIHK LNRDDSDVH
251 SPRYSFSDDT KSPLSVPRSK SEMNYIEGK VVKRSATLPL PARSSSLKSS
301 PERNDWEPLD KKVDTRKYRA EPKSIYEYQP GKSSVLNEK MSRDISPEEI
351 DLKNEPWYKF FSELEFRPS SAVSPTPDIT SEPPGYIYSS NFHAVKRESO
401 GTPGGLASLE NERQIYKSVL EGGDIPLQGL SGLKRPSSSA STKDSSEPRH
451 FIPADYLEST EEFIRRRHDD KEKLLADQRR LKREQUEEADI AARRHTGVIP
501 THHQFITNER FGDLLNIDDT AKRKSGLMR PARAKDFKA QTLKELPLQK
551 GDVVYIYRQI DQNWYEGEH GRVGIFPTY IELLPPAEKA QPRKLAPVQV
601 LEYGEAIAKF NFNGDTQVEM SFRKGERITL LRQVDENWYE GRIPGTSRQG
651 IFPITYVDVL KRPLVKTPVD YIDL PYSSSP SRSATVSPQA SHHLSAGPD
701 LTESSEKNYVQ PQAQRRVTP DRSQPSLDC SYQALYSYVP QNDELELRD
751 GDIVDMKCC DDGWFVGTSR RTRQFGTFPG NYVKPLYL (SEQ ID NO: 30)

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FIG. 43

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1 CCTCACCGNN CCTGGTGTAG GTACCGGATC GAATTCAAGC GAAAAACAGA
51 GCGGGGCTGA CTGTAGCGTG GAGCGCGAGC CGGGCTGGAC GCGCGCAAGC
101 CCTTGCCGGG GACCCGCGAG GCAAGCAGTC TCCCTGTGGA GCGTCGTCCT
151 CCATCCCTGT AAGCACCGTT ACAGAGAATG AAACAAGGGC AGAAGTTACA
201 GAGCCCGTGA GGCATCTTCA AATAGAAGAC TGGAGACTAG AAASAGAATA
251 TTGCCAGGAG TTGGCATCCA TTGGAAGACC TTGAGATCCT CTCAGCTCAC
301 AACTCCAGGA CCGATGCATC TTCCCACCAC CTTGAAGCAC TGAGCCCTCC
351 AGAGCTGCAT CTGGGAAGAC TCGCCTGCCT CCAGCATGAG TTCTGAATGT
401 GATGTTGGAA GCTCTAAAGC TGTGGTGAAT GGCTTGGCAT CTGGCAACCA
451 TGGACCAGAC AAAGACATGG ACCCTACCAA AATCTGCACT GGGAAAGGAA
501 CAGTGACTCT TCGGGCCTCG TCTTCCTACA GGGGAACCCC AAGCAGCAGC
551 CCTGTGAGCC CCCAGGAATC TCCGAAGCAT GAAAGCAAGT CAGATGAATG
601 GAAACTTTCT TCCAGTGCAG ATACCAATGG CAACGCCAG CCCTCCCCAC
651 TTGCTGCCAA GGGCTATAGA AGTGTGCATC CCAGCCTTTC TGCTGACAAG
701 CCCCAGGGCA GTCCTTTACT AAACGAAGTT TCTTCTTCCC ACATTGAAAC
751 CGATTCCCAA GACTTCCCTC CAACAAGCAG ACCTTCGTCT GCCTACCCCT
801 CCACCACCAT CGTCAACCTT ACCATTGTGC TCCTGCAGCA CAATCGAGAG
851 CAGCAAAAGC GACTCAGTAG TCTTTCAGAT CCTGCCTCAG AGAGAAGAGC
901 GGGTGAGCAG GACCCAGTAC CAACCCAGC AGAACTACT TCGCCCGGCA
951 GGGCTTCTGA GAGAAGGGCA AAGGATGCTA GCAGACGGGT GGTGAGGAGC
1001 GCACAGGACC TGAGCGATGT GTCTACAGAT GAAGTGGGCA TTCCACTCCG
1051 GAATACCGAG CGATCGAAAG ACTGGTACAA AACTATGTTT AAACAGATCC
1101 ACAAAGTAA CAGAGATGAT GATTCTGATG TCCATTCCCC TCGATACTCC
1151 TTCTCTGATG ACACAAAGTC TCCCCTTTCT GTGCCTCGCT CAAAAAGTGA
1201 GATGAACTAC ATCGAAGGGG AGAAAGTGGT TAAGAGGTCC GCCACACTCC
1251 CCCTCCCAGC CCGCTCTTCC TCACTCAAGT CCAGCCCGGA AAGAAACGAC
1301 TGGGAGCCCC TAGATAAGAA AGTGGATACG AGAAAATACC GAGCAGAGCC
1351 CAAAAGCATT TACGAATATC AGCCGGGCAA GTCTTCGGTC CTGACCAATG
1401 AGAAGATGAG TCGGGATATA AGCCAGAAG AGATAGATTT AAAGAATGAA
1451 CCTTGGTATA AATTCTTTTC GGAATTGGAG TTTGGGAGAC CGAGCTCAGC
1501 AGTCAGCCCG ACTCCAGACA TTACGTCAGA GCCTCCTGGA TATATCTATT
1551 CTTCCAACTT CCATGCAGTG AAGAGAGAAT CGGACGGGAC CCCCAGGGGT
1601 CTCGCTAGCT TGGAGAATGA GAGGCAGATC TATAAGAGTG TCTTGAAGC
1651 TGGCGACATC CCTCTTCAGG GCCTCAGTGG GCTCAAGCGA CCTTCCAGCT
1701 CAGCTTCCAC TAAAGATTCA GAGTCACCAA GACATTTTAT ACCAGCTGAT
1751 TACTTGGAGT CCACAGAAGA ATTTATTCGG AGACGGCACG ATGATAAAGA
1801 GAAACTTTTA GCGGACCAGA GACGACTTAA GCGCGAGCAA GAAGAGGCCG
1851 ATATTGCAGC TCGCCGCCAC ACAGGTGTCA TCCCGACTCA TCATCAGTTT
1901 ATACTAATG AGCGCTTTGG GGACCTCCTC AATATAGATG ATACGGCCAA
1951 AAGGAAATCT GGGTTAGAGA TGAGACCTGC TCGAGCCAAA TTTGACTTTA
2001 AAGCCCAGAC CCTGAAGGAG CTGCCTCTGC AGAAGGGAGA CGTTGTTTAC
2051 ATCTACAGAC AGATTGACCA GAACTGGTAT GAAGGTGAAC ACCATGGCCG
2101 GGTGGGAATC TTCCCACGCA CCTATATCGA GCTTCTTCTT CCAGCTGAGA
2151 AGGCTCAGCC CAGAAAGTTG GCACCCGTAC AAGTTTTGGA ATATGGAGAA

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FIG. 42A

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2201 GCCATTGCAA AGTTTAACTT TAATGGAGAT ACACAAGTAG AAATGTCTTT
2251 CCGAAAGGGG GAGAGGATCA CGCTGCTCCG ACAGGTGGAT GAGAACTGGT
2301 ATGAAGGGAG GATTCCTGGG ACATCTCGCC AAGGCATTTT CCCTATCACC
2351 TATGTAGATG TGCTTAAGAG GCCATTGGTG AAAACCCCTG TGGATTACAT
2401 CGACCTGCCT TATTCTTCTT CCCCAGTCG CAGTGCCACT GTGAGCCCAC
2451 AGGCTTCTCA TCATTCATTG AGCGCAGGAC CTGATCTCAC AGAATCTGAA
2501 AAGAACTATG TGCAACCTCA AGCCCAGCAG CGAAGAGTCA CCCAGACAG
2551 GAGTCAGCCC TCACTGGATT TGTGTAGCTA CCAAGCGTTA TATAGTTATG
2601 TGCCACAGAA CGATGATGAG TTGGAACTCC GAGATGGAGA TATTGTTGAT
2651 GTCATGGAAA AATGTGACGA TGGATGGTTT GTTGGCACTT CGAGAAGGAC
2701 GAGGCAGTTT GGTACTTTTC CAGGCAACTA TGTA AACCT TTATATCTAT
2751 AAGAAGACTA AAAAGCACAG AGATTATTTT TTATCGGAGG ATGAAGCATC
2801 ATTCATGAAC TGGTCTCTTT ATTTAAGTAC TGAGTCAGTA AGAAAACTAA
2851 TGCAGTTGGT AAAGAAAGAA TTCAAAGAAG GAACAGAGAA GTGTGTTTGA
2901 AACCCATTGT GTATCAGGGA TTA ACTATCT GCTGAAGACA TCTGTATTTA
2951 CATGACTGCT TCTGGGAGCT GCTCTAGCCC CCGCTGCTTG GGAATCTGA
3001 TCTGGAGCAT GTCCATGAGC AACATTAGCC AAAAAAAAAA GCTTGGGCCC
3051 TATTCTATAG TGTCACCTAA ATACTAGCTT GATCCGGCTG CTAACAAAGC
3101 CCGAAAGGAA GCTGAGTTGC TGCTGCCACC GCTGAGCAAT AACTAGCATA
3151 ACCCCTTGGG GCCTCTAAAC GGGTCTTGAG GGGTTTTTTG GCTGAAAGGA
3201 GGA ACTATAT CCGGATAACC TGGCGTAATA GCGAAGAGGC CCGCACC GAT
3251 CGCCCTTCCC AACAGTTGGG CAGCCTGAAT GGCGAATGGA CGCGCCCTGT
3301 AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGCGCA GGGTG

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(SEQ ID NO:29)

FIG. 42B

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1 TTNNCACTCA CCGTCCTGGT GATGGTACCG GATCGAATTC AAGCGTGGCC
51 GTGGCCGTGG GGCGCGCGGG GACCGCCCGG GGTGCCCCGCT CCGCTCAGCG
101 TCCGGGCGCG GTGGTCCGGC GGAGCCCCGA GACCACCCCG GGGCGGGGCG
151 CCGCCGCGAT GTCGGTGGCT GGGCTCAAGA AGCAGTTCCA CAAAGCCAGC
201 CAGCTGTTTA GTGAAAAAAT AAGTGGTGCC GAAGGAACGA AGCTAGATGA
251 AGAATTTCTG AACATGGAAA AGAAAATAGA TATCACCAGT AAAGCTGTTG
301 CAGAAATCCT TTCAAAGGCC ACAGAGTATC TCCAACCCAA TCCAGCATA
351 AGAGCTAAGC TAGGAATGCT GAACACTGTG TCGAAGCTCC GAGGGCAGGT
401 GAAGGCCACC GGCTACCCAC AGACGGAAGG CTTGCTGGGG GACTGCATGC
451 TGAAGTATGG CAAGGAGCTC GGAGAAGACT CTGCTTTTGG CAACTCGTTG
501 GTAGATGTTG GTGAGGCCCT GAAACTCATG GCTGAGGTGA AAGACTCTCT
551 GGATATTAAT GTGAAGCAAA CTTTTATTGA CCCACTGCAG CTACTGCAAG
601 ACAAAGATTT AAAGGAGATC GGGCACCACC TGAGAAAGCT GGAAGGCCGT
651 CGCCTGGATT ATGATTATAA AAAGCGGCGG GTAGGTAAGA TCCCCGAGGA
701 AGAAATCAGA CAAGCAGTAG AGAAGTTTGA AGAGTCAAAG GAGTTGGCCG
751 AAAGGAGCAT GTTTAATTTT TTAGAAAATG ATGTAGAGCA AGTGAGCCAG
801 CTGGCTGTGT TTGTAGAGGC GGCATTAGAC TATCACAGGC AGTCCACAGA
851 GATCCTCCAG GAGCTGCAGA GCAAGCTGGA GTTGCGAATA TCTCTGCA
901 CCAAAGTCCC CAAGCGAGAA TTCATGCCAA AGCCTGTGAA CATGAGTTCC
951 ACCGATGCCA ATGGGGTCGG ACCCAGCTCT TCATCAAAGA CACCAGGTAC
1001 TGACACTCCC GCGGACCAGC CCTGCTGTCG TGGTCTCTAT GACTTTGAGC
1051 CAGAAAATGA AGGAGAATTA GGATTTAAAG AAGGGGACAT CATTACATTA
1101 ACCAATCAGA TAGATGAAAA CTGGTATGAA GGGATGCTTC GTGGGGAATC
1151 CGGCTTCTTC CCCATTAATT ACGTGAAGT CATTGTGCCT TTACCTCCGT
1201 AAATGTGTCT TTTGGACCTA ACTTCAGAAC TGAAATGAAT TGGCACCAGT
1251 GCTCTCTCAG TGTGGTGTTT TGTGACANCC TCGCTCTCTG GCCCACTTAA
1301 TCACTTTTGT ATGTGTGTTT TCTTTATAAT GTATTTTGTG TCAATTTAAT
1351 TTGTATAACT GATTTCTTTG TCCTAACTCA TAAAAATAGT TTTCTTCTTG
1401 TTCTAAAAAG TCATTGGTTA AATGTATTTG CTTCTGTGTG CTAAACGAG
1451 TAAATTGCGC CCATTCGAAT GGCCTGGGTA GTCCTTGACT GCAGTGGGAA
1501 CGCACCCCTT GCAGCCATGA AAGCTAAAGG TTTGTTTCCT GACATTATTG
1551 ATGGCCTCTG GTCTTTTCCT GTTTTAAGCT TACCTGTGAA CAGCCCAATA
1601 AACNTGACAC ACTGTANAAT AANAAGGGTG GCCCNA (SEQ ID NO:31)

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FIG. 44

1 MSVAGLKKQF HKASQLFSEK ISGAEGTKLD EEFLNMEKKI DITSKAVAEI
51 LSKATEYLQP NPAYRAKLG M LNTVSKLRGQ VKATGYPQTE GLLGDCMLKY
101 GKELGEDSAF GNSLVDVGEA LKLMAEVKDS LDINVKQTFI DPLQLLDQKD
151 LKEIGHHLRK LEGRRLDYDY KKRRVGKIPE EEIRQAVEKF EESKELAERS
201 MFNFLENDVE QVSQLAVFVE AALDYHROST EILQELQSKL ELRISLASKV
251 PKREFMPKPV NMSSTDANGV GPSSSSKTPG TDTPADQPCC RGLYDFEPEN
301 EGELGFKEGD IITLTNQIDE NWYEGMLRGE SGFFPINYVE VIVPLPP

(SEQ ID NO:32)

FIG. 45

1 MSGSYDEASE EITDSFWEVG NYKRTVKRID DGHRLCNDLM SCVQERAKIE
51 KAYAQQLTOW AKRWRQLIEK GPQYGS LERA WGAMMTEADK VSELHQEVKN
101 SLLNEDLEKV KNWQKDAYHK QIMGGFKETK EAEDGFRKAQ KPWAKKMKEL
151 EAAKKAYHLA CKEERLAMTR EMNSKTEQSV TPEQQKKLVD KVDKCRQDVQ
201 KTQEKYEKVL EDVGKTTPOY MEGMEQVFEQ COQFEEKRLV FLKEVLDDIK
251 RHLNLAENSS YMHVYRELEQ AIRGADAQED LRWFRSTSGP GMPMNWPQFE
301 EWNPDLPHTT AKKEKQPKKA EGATLSNATG AVESTSQAGD RGSVSSYDRG
351 QTYATEWSDD ESGNPFGGNE ANGGANPFED DAKGVRVRAL YDYGQEQQDE
401 LSFKAGDELT KLGEEDQGW CRGRLDGSQL GLYPANYVEA I

(SEQ ID NO:34)

FIG. 47

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1 CGGGCTTGAG GCTGGGCCGC CGCCGCCGCC CGCTTTGCCA CCCGCCCCGC
51 TGATGGTGTC CGGTGCTCCG GCGCCCAGGG ACACAGACCG GGAGCAGGAC
101 CACTTCTCTC ACCTCCGGAT CTCTCCTGCT TCCGCAGCCT GTGAGCAGCA
151 GGCCTGCTAA CTGCAGATCC ACAACCGCAC AGCTCGCTAC AGGTGCACCA
201 TGTCTGGCTC CTACGATGAG GCCTCAGAGG AGATCACAGA TAGCTTCTGG
251 GAGGTGGGGA ACTACAAGCG GACGGTGAAG CGCATCGACG ATGGGCACCG
301 CCTGTGCAAC GACCTCATGA GCTGCGTGCA GGAGCGCGCC AAGATCGAGA
351 AGGCATACGC GCAGCAGCTC ACCGACTGGG CCAAGCGCTG GCGCCAGCTC
401 ATCGAGAAAG GTCCTCAGTA TGGCAGCCTG GAGCGGGCGT GGGGCGCCAT
451 GATGACAGAA GCAGATAAGG TCAGCGAGCT GCACCAGGAG GTGAAGAACA
501 GCCTGTGTAA TGAGGACCTG GAGAAAGTCA AGAACTGGCA GAAGGATGCC
551 TATCACAAGC AGATCATGGG TGGCTTCAAG GAGACGAAAG AGGCCGAGGA
601 TGGCTTCCGA AAGGCCCAGA AGCCCTGGGC TAAAAAGATG AAGGAGCTAG
651 AGGCGGCCAA GAAGGCCTAT CACTTGGCTT GTAAGGAGGA AAGGCTGGCC
701 ATGACCCGGG AGATGAACAG TAAGACAGAG CAGTCGGTCA CCCCTGAACA
751 GCAGAAGAAA CTTGTGGACA AAGTGGACAA ATGCAGACAG GATGTGCAAA
801 AGACTCAGGA GAAGTATGAG AAGGTCCTGG AAGATGTGGG CAAGACCACA
851 CCACAGTACA TGGAGGGCAT GGAGCAGGTG TTTGAGCAGT GCCAGCAGTT
901 TGAGGAGAAG CGGCTGGTCT TCCTGAAGGA AGTCCTGCTG GATATCAAAC
951 GGCATCTCAA CCTAGCGGAG AACAGCAGCT ACATGCATGT CTACCGAGAA
1001 CTGGAGCAGG CCATCCGGGG GGCCGATGCC CAGGAGGACC TCAGGTGGTT
1051 CCGCAGCACC AGTGGCCCCG GGATGCCCAT GAACTGGCCG CAGTTCGAGG
1101 AGTGGAACCC AGACCTCCCG CACACCACTG CCAAGAAGGA GAAACAGCCT
1151 AAGAAGGCAG AGGGGGCCAC CCTGAGCAAT GCCACTGGGG CTGTAGAATC
1201 CACATCCCAG GCTGGGGACC GTGGCAGTGT TAGCAGCTAT GACCGAGGCC
1251 AAACATATGC CACCGAGTGG TCAGACGATG AGAGCGGAAA CCCCTTCGGG
1301 GGCAATGAGG CCAATGGTGG CGCCAACCCC TTCGAGGATG ATGCCAAGGG
1351 AGTTCGTGTA CGGGCACTCT ATGACTACGA CGGTCAGGAG CAGGATGAGC
1401 TCAGCTTCAA GGCCGGAGAT GAGCTACCA AGCTCGGAGA GGAAGACGAA
1451 CAGGGTTGGT GCCGCGGGCG GCTGGACAGC GGACAGCTGG GCCTCTATCC
1501 TGCCAACTAC GTTGACGCTA TATAGCTACC TTGCCACCC GACTCCTCTC
1551 AGTCCTTGTC CACCGCCTTC CACCCTTCCC CTCCCCCTTG CCATAGAGTT
1601 CCAGACATAT TTTCCCATCA AGCTTTTATT TTTTAAAAG TCAAAACAGA
1651 ACAAAAAAAAA AAAAAAAAAA GAAGAAATAC GAAGAGACAG CGTTTGCAGC
1701 CTACCTGGAG GCCGGGGGGG AGGGGGCTTA GGGTGATGGC CTCCCCCACA
1751 GCGTGGGCAA GGATCTTGGG ACTAACCCAA TGTCACATCT GGTCTATAGA
1801 GTCCACCAAA GAGTCTCCTG AGTCTTGAGG GAGATCTTCT GGATCCTTCT
1851 ACCCTGTCTC GCTCTCCTAT CCCACCACAG CTGCCAGCAG CTGCCCATGT
1901 CACCTGAGCC TGGCTTCTTA AACTCTCCTG TCCCCTCTCC TGTCCCCCTT
1951 CAACGCCCCC TTCTCTTAAA GGGCCCCCAA TCTTTAGTCT TCCACTCTGC
2001 CCTGGGGGTG CTTTTCTCTT CCCAGCCCTG TCCAGTGAGG CTGGGGGAGA
2051 AGGCTGCGGA GGGGAGGGGA GTGTCTCTTC ACTCCCCAG ACATGAAGGC
2101 AGGTGAGTGG GAGGGAGTCA TGGCCTCCCT GGCATACAGG AGAGGAAGAA
2151 GGAGAACAGA CCATCTGACC AGGCTGTGCA ACACTCCCAA TGCCAAGCCC

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FIG. 46A

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2201 ATTTGAGGGA TGA AACCT AGCTGGGCCT GTGGGCAGAG GGCTCCTCCT
2251 CAGAGCCAAT GAGCATTTGC AGAGACCCTA CCTGTCTCTT TAGTCCTTGG
2301 CAATGGGCAA AGCCTCTTCC TTGAAAAGTC CAGGGCAAAG CCAGCAACAG
2351 TAGCAACCTC CTCTCACTCT GGGGAGGAGG CATTGGCCAC CCATCCCCCT
2401 CCCTTCATGG TCATTCAGAA ACGCCACAGC CCCTCCCATC CCCAATCACT
2451 GTGTCAGCAT CAGCCTTTGT GAAGACGGTC TACAAGGCTC TCACCTGGCC
2501 AACCTAGGAG ATTCAGGGGC TCAGGAACCT AGGAGATTCA GGGGCTTGGG
2551 GAACCTCCAC CTTGGCACTG TAAGGGGAAG CCAGCAGCTC AGGCTGGTGT
2601 GAGGAAGGAA CTCTGGATGG TCACTGTAGC TTTCTTCCTT GACCTTTTAG
2651 TCCCCAACAT CCCCTCTGAA TGCTGGCAGC ACCCCACCC CCACACACAC
2701 ACTCCCATT CTCTAAGCCC GAGAGTCTTG AGTCTTCATT AAAGGATTCT
2751 GGGTGTGGGA GGGGACACAG GGCCTTGTGG TTGGGAAGCA GGTGGCAGGC
2801 TCTCCCTTGG GAGGATGGGG TGGGAAACGA AACAGGTCAA CCAAGACCTC
2851 TTACAGTGGA AAGTGGTCAG AGGCTGTTTC TTTGGACCTT TGGGAACACA
2901 GATTTGAGAA AGTCTCATAT TCACAGCTGG TGTCCGCTAG GCCTCTGGCC
2951 TACGGACACC CTCTGCCTTG TGAATCAGGT GACCTTTTGG GCCTCCAGGG
3001 AAAGAACAGG ACCACCATCC ATGTTCTCCG CGTCCCTTTA GCTCTCTGCT
3051 GCTTCTCCTG ACACTCAGGT CATGGACCCA AGCTTTGGGG TCCTGACCAC
3101 CGCCCCCCCC CACCCCCCTT CTCTTGACTA GGCTGCAGCA GGGCCTTCTG
3151 TTGGGTCAGT CCTCCTCAGG GCCAGGAGCA GGAACCTAGC ACTCAAGAGA
3201 CAGGGCTGTA AGCACCCACT TCCCTGTCAC TGTTTGCCCT TGGGGCTTCA
3251 GCTGCAGCCC AGGTTGGGCC CTGGAGCCCT CAGAACCGGA AGCAGGATTC
3301 AAACCTCCCC TTCTCCACAG CCCCCCCTGC CTCCCCAGAT GGTAGACATC
3351 CCCAGCTCT TACCTTCACC CTCATCTCAG AAAGGCAAGA AGCCGCCATG
3401 TCCGCACCTT GGGGCCTGGG CTTCCCCCTC TCTGTGCCAG CGGTTCCAG
3451 CACCTGGGGA GGGGCTGTGG CCTGACCAGA CCCCAGGCC ACCCCACATA
3501 GTATACTAGC TGCCCACTCT GGGGCAGGAA CTGGAAAATC CATCCCTTTT
3551 GAACAACCAC CTTCAATGAC CCCCCCATC TGGGACCAGA CTTGGTCCTC
3601 AAGTTATTCA GCACCCCCAG TGCAGGAGGG TCCTCCCCC ACCCCCCGAA
3651 GTCCCTGGAG CCCGGAGCAG AGCCCCACCT GTGATTCCTG GTGTTAGGGC
3701 ACCTCAAACC TTGGGCTGGA CCACACCCT TCCCGCCATT TCCAGACCCC
3751 TACCTGTACT CCCAGTGCT CCCCAGGGGC CTCTTGATGC TGCACGGGAC
3801 CCTGCAGGGC TCGGTCAGTG ATGTGTTTTG TCCCAGTTA ACCGCCATCC
3851 AGCGACCTGG TTCCAGGAGG AGCTCAGGTC ACCCCACCA CCGCCGCCAC
3901 TGCCTCTGCC GCCCTAGGCT TTCAGACATC ATTAGTTCCG ACACTTGTGA
3951 AACTCCGAGA CGTGCCGTGG TCTCAGCAAT GCACCTGTTT TATACATGAT
4001 TGTGTAATTT AAAGGTATAT AAATACAAAT ATATATATTA TATCTATATC
4051 TATCAGTTGT GACCGTATGG CTGTCGATAA AACCAGAATT C

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(SEQ ID NO:33)

FIG. 46B

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1   GAATTCGTCG ACCCACGGTC CGGGAAGCCT TTCACAAGCA GATGATGGGC
51  GGCTTCAAGG AGACCAAGGA AGCTGAGGAC GGCTTTCGGA AGGCACAGAA
101 GCCCTGGGCC AAGAAGCTGA AAGAGGTAGA AGCAGCAAAG AAAGCCCACC
151 ATGCAGCGTG CAAAGAGGAG AAGCTGGCTA TCTCACGAGA AGCCAACAGC
201 AAGGCAGACC CATCCCTCAA CCCTGAACAG CTCAAGAAAT TGCAAGACAA
251 AATAGAAAAG TGCAAGCAAG ATGTTCTTAA GACCAAAGAG AAGTATGAGA
301 AGTCCCTGAA GGAACCTGAC CAGGGCACAC CCCAGTACAT GGAGAACATG
351 GAGCAGGTGT TTGAGCAGTG CCAGCAGTTC GAGGAGAAAC GCCTTCGCTT
401 CTTCCGGGAG GTTCTGCTGG AGGTTTCAGAA GCACCTAGAC CTGTCCAATG
451 TGGCTGGTTA CAAAGCCATT TACCATGACC TGGAGCAGAG CATCAGAGCA
501 GCTGATGCAG TGGAGGACCT GAGGTGGTTC CGAGCCAATC ACGGGCCGGG
551 CATGGCCATG AACTGGCCGC AGTTTGAGGA GTGGTCCGCA GACCTGAATC
601 GAACCCTCAG CCGGAGAGAG AAGAAGAAGT CCACTGACGG CGTCACCCTG
651 ACGGGCATCA ACCAGACAGG CGACCACTCT CTGCCGAGTA AGCCCAGCAG
701 CACCCTTAAT GTCCCGAGCA ACCCCGCCCC GTCTGCGCAG TCACAGTCCA
751 GCTACAACCC CTTGAGGAT GAGGACGACA CGGGCAGCAC CGTCAGTGAG
801 AAGGACGACA CTAAGGCCAA AAATGTGAGC AGCTACGAGA AGACCCAGAG
851 CTATCCCACC GACTGGTCAG ACGATGAGTC TAACAACCCC TTCTCCTCCA
901 CGGATGCCAA TGGGGACTCG AATCCATTCTG ACGACGACGC CACCTCGGGG
951 ACGGAAGTGC GAGTCCGGGC CCTGTATGAC TATGAGGGGC AGGAGCATGA
1001 TGAGCTGAGC TTCAAGGCTG GGGATGAGCT GACCAAGATG GAGGACGAGG
1051 ATGAGCAGGG CTGGTGCAAG GGACGCTTGG ACAACGGGCA AGTTGGCCTA
1101 TACCCGGCAA ATTATGTGGA GCGATCCAG TGA (SEQ ID NO:35)

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FIG. 48

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1   RIRRPTVREA FHKQMMGGFK ETKEAEDGFR KAQKPWAKKL KEVEAAKKAH
51  HAACKEECLA ISREANSKAD PSLNPEQLKK LQDKIEKCKQ DVLKTKEYE
101 KSLKELDQGT PQYMENMEQV FEQCQFEEK RLRFFREVLL EVQKHLDSL
151 VAGYKAIYHD LEQSIRAADA VEDLRWFRAN HPGMAMNWP QFEWSADLN
201 RTLSRREKKK STDGVTLTGI NQTGDQSLPS KPSSTLNVPS NPAQSAQSQS
251 SYNPFEDDD TGSTVSEKDD TKAKNVSSYE KTQSYPTDWS DDESNNPFSS
301 TDANGDSNPF DDDATSGTEV RVRALYDYEG QEHDLSFKA GDELTKMEDE
351 DEQGWCKGRL DNGQVGLYPY NYVEAIQ (SEQ ID NO:36)

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FIG. 49

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1          AAAGGGAGG AGAGTGTCAA AAAGAAGGAT
30 GCGGAGGAAA AAGGCAAACA GGAAGCACAA GACAAGCTGG
70 GTCGGCTTTT CCATCAACAC CAAGAACCAG CTAAGCCAGC
110 TGTCCAGGCA CCCTGGTCCA CTGCAGAAAA AGGGTCCACT
150 TACCATTCTT GCACAGGAAA ATGTAAAAGT GGTGTATTAC
190 CGGGCACTGT ACCCCTTTGA ATCCAGAAGC CATGATGAAA
230 TCACTATCCA GCCAGGAGAC ATAGTCATGG TGGATGAAAG
270 CCAAAGTGA GAACCCGGCT GGCTTGGAGG AGAATTAATA
310 GGAAAGACAG GGTGGTTCCC TGCAAACCTAT GCAGAGAAAA
350 TCCCAGAAAA TGAGGTTCCC GCTCCAGTGA AACCAGTGAC
390 TGATTCAACA TCTGCCCCTG CCCCCAACT GGCCTTGCCT
430 GAGACCCCCG CCCCTTTGGC AGTAACCTCT TCAGAGCCCT
470 CCACGACCCC TAATAACTGG GCCGACTTCA GCTCCACGTG
510 GCCCACCAGC ACGAATGAGA AACCAGAAAC GGATAACTGG
550 GATGCATGGG CAGCCCAGCC CTCTCTCACC GTTCCAAGTG
590 CCGGCCAGTT AAGGCAGAGG TCCGCCTTTA CTCCAGCCAC
630 GGCCACTGGC TCCTCCCCGT CTCCTGTGCT AGGCCAGGGT
670 GAAAAGGTGG AGGGGCTACA AGCTCAAGCC CTATATCCTT
710 GGAGAGCCAA AAAAGACAAC CACTTAAATT TTAACAAAAA
750 TGATGTCATC ACCGTCCTGG AACAGCAAGA CATGTGGTGG
790 TTTGGAGAAG TTCAAGGTCA GAAGGGTTGG TTCCCCAAGT
830 CTTACGTGAA ACTCATTTCA GGGCCCATAA GGAAGTCTAC
870 AAGCATGGAT TCTGGTTCTT CAGAGAGTCC TGCTAGTCTA
910 AAGCGAGTAG CCTCTCCAGC AGCCAAGCCG GTCGTTTCGG
950 GAGAAGAAAT TGCCCAGGTT ATTGCCTCAT ACACCGCCAC
990 CGGCCCCGAG CAGCTCACTC TCGCCCCTGG TCAGCTGATT
1030 TTGATCCGAA AAAAGAACCC AGGTGGATGG TGGGAAGGAG
1070 AGCTGCAAGC ACGTGGGAAA AAGCGCCAGA TAGGCTGGTT
1110 CCCAGCTAAT TATGTAAAGC TTCTAAGCCC TGGGACGAGC
1150 AAAATCACTC CAACAGAGCC ACCTAAGTCA ACAGCATTAG
1190 CGGCAGTGTG CCAGGTGATT GGGATGTACG ACTACACCGC
1230 GCAGAATGAC GATGAGCTGG CCTTCAACAA GGGCCAGATC
1270 ATCAACGTCC TCAACAAGGA GGACCCTGAC TGGTGGAAG
1310 GAGAAGTCAA TGGACAAGTG GGGCTCTTCC CATCCAATTA
1370 TGTGAAGCTG ACCACAGACA TGGACCCAAG CCAGCAATGA
      (SEQ ID NO: 37)

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FIG. 50

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1   KGRRVSKRRM ARKKANRKHK TSWVGFSINT KNQLSQLSRH
41  PGPLOKKGPL TISAQENVKV VYYRALYPFE SRSHDEITIQ
81  PGDIVMVDES QTGEPGWLGG ELKGKTGWFP ANYAEKIPEN
121 EVPAPVKPVT DSTSAPAPKL ALRETPAPLA VTSSEPSTTP
161 NNWADFSSTW PTSTNEKPET DNWDAAWAAP SLTVPSAGQL
201 RQRSAFTPAT ATGSSPSPVL GQGEKVEGLQ AQALYPWRAK
241 KDNHLNFNKN DVITVLEQQD MWWFGEVQGO KGWFPKSYVK
281 LISGPIRKST SMDSGSSESP ASLKRVASPA AKPVVSGEEI
321 AQVIASYTAT GPEQLTLAPG QLILIRKKNP GGWWEGELQA
361 RGKKRQIGWF PANYVKLLSP GTSKITPTEP PKSTALAAVC
401 QVIGMYDYTA QNDELAFNK GQIINVLNKE DPDWWKGEVN
441 GQVGLFPSNY VKLTTDM DPS QQ (SEQ ID NO:38)

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FIG. 51

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1   GAATTCGCGG CCGCGTCGAC CAAGATCATT CCTGGGAGTG
41  AAGTAAACG GGAAGAACCA GAAGCTTTGT ATGCAGCTGT
81  AAATAAGAAA CCTACCTCGG CAGCCTATTC AGTTGGAGAA
121 GAATATATTG CACTTTATCC ATATTCAAGT GTGGAACCTG
161 GAGATTTGAC TTTCACAGAA GGTGAAGAAA TATTGGTGAC
201 CCAGAAAGAT GGAGAGTGGT GGACAGGAAG TATTGGAGAT
241 AGAAGTGGAA TTTTCCATC AAACATGTC AAACCAAAGG
281 ATCAAGAGAG TTTTGGGAGT GCTAGCAAGT CTGGAGCATC
321 AAATAAAAAA CCTGAGATTG CTCAGGTAAC TTCAGCATAT
361 GTTGCTTCTG GTTCTGAACA ACTTAGCCTT GCACCAGGAC
401 AGTTAATATT AATTCTAAAG AAAAATACAA GTGGGTGGTG
441 GCAAGGAGAG TTACAGGCCA GAGGAAAAAA GCGACAGAAA
481 GGATGGTTTC CTGCCAGTCA TGTAAACTT TTGGGTCCAA
521 GCAGTGAAAG AGCCACACCT GCCTTTCATC CTGTATGTCA
561 GGTGATTGCT ATGTATGACT ATGCAGCAAA TAATGAAGAT
601 GAGCTCAGTT TCTCCAAGGG ACAACTCATT AATGTTATGA
641 ACAAAGATGA TCCTGATTGG TGGCAAGGAG AGATCAACGG
681 GGTGACTGGT CTCTTTCCTT CAACTACGT TAAGATGACG
721 ACAGACTCAG ATCCAAGTCA ACAGTGA (SEQ ID NO:39)

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FIG. 52

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1 EFAAASKII PGSEVKREEP EALYAAVNKK PTSAAYSVGE
41 EYIALYPYSS VEPGDLTFTE GEEILVTQKD GEWWTGSIGD
81 RSGIFPSNYV KPKDQESFGS ASKSGASNKK PEIAQVTSAY
121 VASGSEQLSL APGQLILILK KNTSGWWQGE LQARGKKRQK
161 GWFPASHVKL LGPSSERATP AFHPVCQVIA MYDYAANNED
201 ELSFSKGQLI NVMNKDDPDW WQGEINGVTG LFPSNYVKMT
241 TSDPSQQ (SEQ ID NO:40)

FIG. 53

HSLHLHRHQGRKERARYDLEAAQDNELTFKAGEIMTVLDDSDPNWWKGETHQGIGLFPSN 60
FVTADLTAEPEMIKTEKKTQVFSDDVQVETIEPEPEPAFIDEDKMDQLLOMLQSTDPSSD 120
QPDLPPELLHLEAMCHQMGPLIDEKLEDIDRKHSELSENVKVMEALSLYTKLMNEDPMYS 180
MYAKLQNPYYMQSSGVSGSQVYAGPPPSGAYLVAGNAQMSHLQSYSLPPEQLSSLSQAV 240
VPPSANPALPSQQTQAAYPNRSPGDLMPGDSECRGSAEDSQMRISPPYFPTGQQA 296
(SEQ ID NO:190)

FIG. 55

IRGRVDQGEWPLPGRGTPGPSGLCVPEDQCRVRDLKGWLSFWAKAEKEE 50
ENRRLEEKRWAEAAQRQLEQERRERELREAAARREORYQEQGGEASPOSRT 100
WEQQQEVVSRNRNEQESAVHPREIFKOKERAMSTTSISSPQPGKLRSPFL 150
QKQLTQPETHFGREPAAAISRPRADLPAEEPAPSTPPCLVQAEAAVYEE 200
PPEQETFYEQPPLVQQQGAGSEHIDHHIQGQGLSGQGLCARALYDYQAAD 250
DTEISFDPENLITGIEVIDEGWWRGYGPDPGHFGMFANYVELIDEAEGTS 300
CPSPLRHGFLIAGRGGLGVDIOHSSRNRTPSEDEASGLPPAWQTQPVTN 350
AAMAW 355 (SEQ ID NO:192)

FIG. 57

GRVDIERKRELEMQKKLEDEAARKAKOGKENLWKENLRKEEEEKQKRLQEEKTOEKIQE 60
EERKAEKQRETASVLVNYRALYPFEARNHDEMSFNSGDI IQVDEKTVGEPGWLYGSFQG 120
NFGWFPCNYVEKMPSSENEKAVSPKKALLPPTVSLSATSTSSEPLSSNQPASVTDYQNV 180
FSNLTVNTSWOKKSAFTRTVSPGSVSP IHGQGVVENLKAQALCSWTAKKDNHLNFSKHD 240
IITVLEQQENWWFGEVHGGRGWFPKSYVKIIPGSEVKREEPEALYAAVNKKPTSAAYSVG 300
EEYIALYPYSSVEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFG 360
SASKSGASNKKPEIAQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQGELOARGKKRQ 420
KGWFPASHVKLLGPSSERATPAFHPVCQVIAMYDYAANNEDLSFSKGQLINVMNKDDPD 480
WWQGEINGVTGLFPSNYVKMTTSDPSQQ 509 (SEQ ID NO:194)

FIG. 59

CACTCTCTACACTTGCACCGGCATCAAGGACGAAAAGAAC 40
 GCGCTAGATATGACTTGGAAGCTGCTCAAGACAATGAACT 80
 TACTTTCAAAGCTGGAGAAATTATGACAGTTCTTGATGAC 120
 AGTGATCCTAACTGGTGGAAAGGTGAAACCCATCAAGGCA 160
 TAGGGTTATTTCTTCTAATTTTGTGACTGCAGATCTCAC 200
 TGCTGAACCAGAAATGATTAACAGAGAAGAAGACGGTA 240
 CAATTTAGTGATGATGTTTCAGGTAGAGACAATAGAACCAG 280
 AGCCGGAACCAGCCTTTATTGATGAAGATAAAATGGACCA 320
 GTTGCTACAGATGCTGCAAAGTACAGACCCAGTGATGAT 360
 CAGCCAGACCTACCAGAGCTGCTTCATCTTGAAGCAATGT 400
 GTCACCAGATGGGACCTCTCATTGATGAAAAGCTGGAAGA 440
 TATTGATAGAAAACATTCAGAACTCTCAGAACTTAATGTG 480
 AAAGTGATGGAGGCCCTTTCCTTATATACCAAGTTAATGA 520
 ACGAAGATCCGATGTATTCCATGTATGCAAAGTTACAGAA 560
 TCAGCCATATTATATGCAGTCATCTGGTGTCTGTTCT 600
 CAGGTGTATGCAGGGCTCCTCCAAGTGGTGCCTACCTGG 640
 TTGCAGGGAACGCGCAGATGAGCCACCTCCAGAGCTACAG 680
 TCTTCCCCCGGAGCAGCTGTCTTCTCTCAGCCAGGCAGTG 720
 GTCCCACCATCCGCAAACCCAGCCCTTCTAGTCAGCAGA 760
 CTCAGGCCGCTTACCCAAACCGCTCCCCAGGGGACCTCAT 800
 GAAGCCCGGTGATTCTGAATGCCGTGGATCTGCCGAGGAT 840
 TCCCAGATGCGTATTTCTCCTCCGTACTTCCCCACAGGAC 880
 AGCAGGCTTGAATAGCTGATTGCCTATGCAGGACAACAGG 920
 CTTGAATAGCTGACTGCCTATGCATTCTCTTTGCTTGCCA 960
 GTTTTTTGGACATCAAACCTTGACAGATCCAAGATTATTAC 1000
 TTTGATCTTCCCCACACCCCTCCCACCCCGAGTCTACTA 1040
 TGGTCCCATCATAGTATTCTGAAAATCAGTGAATGGCCAC 1080
 TCTACCAGTTATTTCTACCAGTTTTTAGGTTCTAAACCTC 1120
 AGGCATTCTGGACTCTTCTGTTCATTATCATATTTTGAAG 1160
 GCATTATCTTCAAATCTATCTAGACTCTGACCCTTTCTC 1200
 CCATCTCCACCATTACTGCCGTGGCTCTTCTGCTGGTCGG 1240
 CTCTCTCCTGGTGGATCCGTAATAACCTGCAGTCAGCTAT 1280
 CCTGGTCCAGAAGGGAACCCCGTTAAACCCTGTTGGAATC 1320
 TTATCACGCTTCTGCTCCAGAACGAACCCAGTCTGTCTGT 1360
 CTCCTCAGAGTGTAAGCTACAGTCCTTATTGTGGCCATC 1400
 AGGTGCTGTGTGTTCTCCAGCCCCCTCCCCACCACCGCAG 1440
 TCCTGCCGGTGATCTTAGCTGCTCTCCCCTCGGAACCCCT 1480
 TGCGGCCCCCTCTGCCGCAACAXTCGTGGCCTGCTGTTCC 1520
 TTGAACATGCTTGGTGTCTTCTCCTCAAAGGCTTCTTT 1560
 CTGTTTACCTGAAATGTACTTGCCTAGGGAAATCTTATCC 1600
 TGGCTCACTCCGCTTACTTTTTTCCACATCTTTGCTTAAA 1640
 GTTATTGCCCTTATTGGAGAAGGCACCCCTACCATAAACT 1680
 AGAAATCCCTTGCCCCCAAGCTGCTCCTTT 1710

(SEQ ID NO:189)

FIG. 54

GAATTCGCGGCCGCGTCGACCAAGGAGAGTGGCCGCTTCC 40
 AGGACGTGGGACCCAGGCCCCAGTGGGCTCTGTGTACCA 80
 GAAGACCAATGCCGTGTCAGAGATTTAAAGGGTTGGTTAG 120
 ACAGCTTCTGGGCCAAAGCAGAGAAGGAGGAGGAGAACCG 160
 TCGGCTGGAGGAAAAGCGGTGGGCCGAGGAGGCACAGCGG 200
 CAGCTGGAGCAGGAGCGCCGGGAGCGTGAGCTGCGTGAGG 240
 CTGCACGCCGGGAGCAGCGCTATCAGGAGCAGGGTGGCGA 280
 GGCCAGCCCCAGAGCAGGACGTGGGAGCAGCAGCAAGAA 320
 GTGGTTTCAAGGAACCGAAATGAGCAGGAGTCTGCCGTGC 360
 ACCCGAGGGAGATTTTCAAGCAGAAGGAGAGGGCCATGTC 400
 CACCACCTCCATCTCCAGTCCTCAGCCTGGCAAGCTGAGG 440
 AGCCCCTTCTGCAGAAGCAGCTCACCCAACCAGAGACCC 480
 ACTTTGGCAGAGAGCCAGCTGCTGCCATCTCAAGGCCCAG 520
 GGCAGATCTCCCTGCTGAGGAGCCGGCGCCAGCACTCCT 560
 CCATGTCTGGTGCAGGCAGAAGAGGAGGCTGTGTATGAGG 600
 AACCTCCAGAGCAGGAGACCTTCTACGAGCAGCCCCACT 640
 GGTGCAGCAGCAAGGTGCTGGCTCTGAGCACATTGACCAC 680
 CACATTGAGGGCCAGGGGCTCAGTGGGCAAGGGCTCTGTG 720
 CCCGTGCCCTGTACGACTACCAGGCAGCCGACGACACAGA 760
 GATCTCCTTTGACCCCGAGAACCTCATCACGGGCATCGAG 800
 GTGATCGACGAAGGCTGGTGGCGTGGCTATGGGCCGGATG 840
 GCCATTTTGGCATGTTCCCTGCCAATTACGTGGAGCTCAT 880
 TGATGAGGCTGAGGGCACATCTTGCCCTTCCCCTCTCAGA 920
 CATGGCTTCCTTATTGCTGGAAGAGGAGGCCTGGGAGTTG 960
 ACATTCAGCACTCTTCCAGGAATAGGACCCCCAGTGAGGA 1000
 TGAGGCCTCAGGGCTCCCTCCGGCTTGGCAGACTCAGCCT 1040
 GTCACCCCAAATGCAGCAATGGCCTGGTGATTCCACACA 1080
 TCCTTCCTGCATCCCCGACCCTCCCAGACAGCTTGGCTC 1120
 TTGCCCTGACAGGATACTGAGCCAAGCCCTGCCTGTGGC 1160
 CAAGCCCTGAGTGGCCACTGCCAAGCTGCGGGGAAGGGTC 1200
 CTGAGCAGGGGCATCTGGGAGGCTCTGGCTGCCTTCTGCA 1240
 TTTATTTGCCTTTTTTCTTTTTCTTTGCTTCTAAGGGGT 1280
 GGTGGCCACCACTGTTTAGAATGACCCTTGGGAACAGTGA 1320
 ACGTAGAGAATTGTTTTAGCAGAGTTTGTGACCAAAGTC 1360
 AGAGTGGATCATGGTGGTTTGGCAGCAGGGAATTTGTCTT 1400
 GTTGGAGCCTGCTCTGTGCTCCCCACTCCATTTCTCTGTC 1440
 CCTCTGCCTGGGCTATGGGAAGTGGGGATGCAGATGGCCA 1480
 AGCTCCACCCCTGGGTATTCAAAAACGGCAGACACAACAT 1520
 GTTCCTCCACGCGGCTCACTCGATGCCTGCAGGCCCCAGT 1560
 GTGTGCCTCAACTGATTCTGACTTCAGGAAAAGTAACACA 1600
 GAGTGGCCTTGGCCTGTTGTCTTCCCCTATTTTCTGTCCC 1640
 AGCTCATCCGTGGTCTGAAGCGCCCGCAATTCCAGCTGAG 1680
 CGGCCGC 1687 (SEQ ID NO:191)

FIG. 56

GCGGCCGCGTCGACATTGAAAGGAAAAGATTAGAACTAAT	40
GCAGAAAAAGAACTAGAAAGATGAGGCTGCAAGGAAAGCA	80
AAGCAAGGAAAAGAAAACCTTATGGAAAGAAAATCTTAGAA	120
AGGAGGAAGAAGAAAAACAAAAGCGACTCCAGGAAGAAAA	160
AACACAAGAAAAAATTCAAGAAGAGGAACGGAAAGCTGAG	200
GAGAAACAACGTGAGACAGCTAGTGTTTTGGTGAATTATA	240
GAGCATTATACCCCTTTGAAGCAAGGAACCATGATGAGAT	280
GAGTTTTAATTCTGGAGATATAATTCAGGTTGATGAAAAA	320
ACCGTAGGAGAACCTGGTTGGCTTTATGGTAGTTTTCAAG	360
GAAATTTTGGCTGGTTTCCATGCAATTATGTAGAAAAAAT	400
GCCATCAAGTGAAAATGAAAAAGCTGTATCTCCAAAGAAG	440
GCCTTACTTCCTCCTACAGTTTCTTTATCTGCTACCTCAA	480
CTTCCTCTGAACCACTTTCTTCAAATCAACCAGCATCAGT	520
GACTGATTATCAAAATGTATCTTTTTCAAACCTAACTGTA	560
AATACATCATGGCAGAAAAAATCAGCCTTCACTCGAACTG	600
TGTCCCCTGGATCTGTATCACCTATTCATGGACAGGGACA	640
AGTGGTAGAAAACTTAAAGCACAGGCCCTTTGTTCTGG	680
ACTGCAAAGAAAGATAACCACTTGAACCTCTCAAAACATG	720
ACATTATTACTGTCTTGGAGCAGCAAGAAAATTGGTGGTT	760
TGGGGAGGTGCATGGAGGAAGAGGATGGTTTCCCAATCT	800
TATGTCAAGATCATTCTGGGAGTGAAGTAAACGGGAAG	840
AACCAGAAGCTTTGTATGCAGCTGTAAATAAGAAACCTAC	880
CTCGGCAGCCTATTCAAGTTGGAGAAGAATATATTGCACTT	920
TATCCATATTCAAGTGTGGAACCTGGAGATTTGACTTTCA	960
CAGAAGGTGAAGAAATATTGGTGACCCAGAAAGATGGAGA	1000
GTGGTGGACAGGAAGTATTGGAGATAGAAGTGAATTTTTT	1040
CCATCAAACCTATGTCAAACCAAGGATCAAGAGAGTTTTG	1080
GGAGTGCTAGCAAGTCTGGAGCATCAAATAAAAAACCTGA	1120
GATTGCTCAGGTAACCTCAGCATATGTTGCTTCTGGTTCT	1160
GAACAACCTTAGCCTTGCACCAGGACAGTTAATATTAATTC	1200
TAAAGAAAAATACAAGTGGGTGGTGGCAAGGAGAGTTACA	1240
GGCCAGAGGAAAAAAGCGACAGAAAGGATGGTTTCCTGCC	1280
AGTCATGTTAACTTTTGGGTCCAAGTAGTGAAAGAGCCA	1320
CACCTGCCTTTCATCCTGTATGTCAGGTGATTGCTATGTA	1360
TGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTCTCC	1400
AAGGGACAACCTCATTAATGTTATGAACAAAGATGATCCTG	1440
ATTGGTGGCAAGGAGAGATCAACGGGGTGAAGTGGTCTCTT	1480
TCCTTCAAACCTACGTTAAGATGACGACAGACTCAGATCCA	1520
AGTCAACAGTGACCCAATGTTGTCTTCCAGTTGTGAAAGC	1560
ACCCAGAGACCCACTATCCAAGTTTCACTCTAGCGTGGA	1600
GGCAGGGCAGGCAGCCCTGATCAAATATCTGCTACACAAT	1640
TCGTTTACTTCGTTTGAATGTTAGAGCCACTTGTGATTAT	1680
TTTTTTGTGTTTCTAACTTACAGTTTAAATTTATTTGTAA	1720

FIG. 58A

AAAGTTAAAGGATAGTGGGTCTTTGTGTGGCTTTCCCTGC 1760
 TGTTCACTCTGGCATCTTTAGCATTTTTCTTCTTTTTTAA 1800
 TTTGATAATTGTAGGTCATTAGCATGCATATTGAGTTTGC 1840
 CGTTATGTGGTGGGAGTTCAAACACACAAAGACCCACTAT 1880
 TTGCACAACTATTCTTACTGGTTTGGAATAGGCTGCCAT 1920
 GCTTTTTTAATGTTATTGCAACATGTGTATTCATTTACAG 1960
 AATTCAGATAAAATTTGCTTATGTTCTGCTATTATGTTTG 2000
 ATCTAATCCTAATCACAGTGAGCTCTTAATTAGCTCAATA 2040
 TGTGGTTTGCCCTCAAGTGTGCACTGTTTATTACTTTTGA 2080
 ATATGCCACTATGAGTACTGACATTTAGATATGTTTAAAG 2120
 GCCAAGAACTGGAAACAGCCATGCCCTGTTTTCTGTGTAT 2160
 TTGGGATGGGAATAACAACATTTTGGGGGGAGCTTTTTTA 2200
 ATCTCAGAGAAGAGGAAAGTGGCCTGCTCTGGCAGGTATG 2240
 TGCAGTGTTTCATTTGTTCCAGTCCCAAGAATGAGCACTG 2280
 TCCTATGGTAGTTTCGCTTAGGATCTTTATGTGCTCTGGGC 2320
 TAATGAAGGTACTGCATCATGTGCTGCAGCGTGTGTATTC 2360
 TTTTTCGATGACCTATAAAGGGATTATTTTTGAGGAATGA 2400
 AAGGCTCCCATCATTGACTGTGAGATGGGAAAAACCTTTC 2440
 CTAGCTTAGAGCATTTATATCTTAATCCATTTTAAAGTCA 2480
 GAGTTCATTGTTACCTGTTTTAATCAGGTGACTACATGTC 2520
 CCAGTATACAAAGGGGCACTGGTTGACATTCTTCTTAATG 2560
 TATTTAGTAAATATCATAAGAAATCCTTTAAGAGTTTAAA 2600
 TGTCCCCAAAACAGACATGCGGGCTCTAGTCAAGAATGAA 2640
 TTAGAGTGAAGGAAAGCTGTGTAACACCTGGCATTCTCT 2680
 GTGTTTCATGGAGCTTCTTTGAGGCTCTAAGATTGATTTTA 2720
 CCATCAGACTTCTCTAATACCTGTTCTTCAACCATATTGG 2760
 CTACTTTGACATAAGAATTTACTTCTTTTCTGGAATGGA 2800
 AAACACTTTAAAAAATAATAACAAACATTATTATAAACTA 2840
 ATATATGTGAGAGGTGACGCGGCCGCGAATTC 2873

(SEQ ID NO:193)

FIG. 58B

GAATTCGTCGACCCACGCGTCCGAAATATAACTGAAGTTGGGGCACCTAC 50
 TGAAGAAGAGGAAGAAAGTGAAAGTGAAGATAGTGAAGACAGTGGTGGGG 100
 AGGAAGAAGATGCAGAGGAGGAAGAGGAAGAGAAAGAGGAAAAATGAATCT 150
 CACAAATGGTCAACCGGTGAAGAATACATCGCTGTTGGAGATTTTACTGC 200
 TCAGCAAGTTGGAGATCTTACATTTAAGAAAGGGGAAATTCTCCTTGTA 250
 TTGAAAAAAACCTGATGGTTGGTGGATAGCTAAGGATGCCAAAGGAAAT 300
 GAAGGTCTTGTTCCAGAACCTACCTAGAGCCTTATAGTGAAGAAGAAGA 350
 AGGCCAAGAGTCAAGTGAAGAGGGCAGTGAAGAAGATGTAGAGGCGGTGG 400
 ATGAAACAGCAGATGGAGCAGAAGTTAAGCAAAGAAGTATCCCCACTGG 450
 AGTGCTGTTCAGAAAGCGATTTAGAGGCGGGCATCTTCTGTCTTGTTAA 500
 TCATGTCTCGTTTTGCTACCTAATAGTTCTGATCCGTCCTAA 543
 (SEQ ID NO:196)

FIG. 60

GAATTCGGCGGACTTCGCGGCCGCGTCGACGAAGAAACCT 40
 GAAGGACACACTAGGCCTCGGCAAGACGCGCAGGAAGACC 80
 AGCGCGCGGGATGCGTCCCCACGCCCAGCACGGACGCCG 120
 AGTACCCCGCCAATGGCAGCGCGCCGACCGCATCTACGA 160
 CCTCAACATCCCGGCCCTTCGTCAAGTTGCGCTATGTGGCC 200
 GAGCGGGAGGATGAGTTGTCCCTGGTGAAGGGGTCGCGCG 240
 TCACCGTCATGGAGAAGTGCAGCGACGGTTGGTGGCGGGG 280
 CAGCTACAACGGGCAGATCGGCTGGTTCCCCTCCAACCTAC 320
 GTCTTGAGGAGGTGGACGAGGCGGTTGCGGAGTCCCCAA 360
 GCTTCCTGAGCCTGCGCAAGGGCGCCTCGCTGAGCAATGG 400
 CCAGGGCTCCCGCGTGCTGCATGTGGTCCAGACGCTGTAC 440
 CCCTTCAGCTCAGTCACCGAGGAGGAGCTCAACTTCGAGA 480
 AGGGGGAGACCATGGAGGTGATTGAGAAGCCGGAGAACGA 520
 CCCCAGTGGTGGAAATGCAAAAATGCCCGGGGCCAGGTG 560
 GGCCTCGTCCCCAAAACTACGTGGTGGTCTCAGTGACG 600
 GGCCTGCCCTGCACCCTGCGCACGCCCCACAGATAAGCTA 640
 CACCGGGCCCTCGTCCAGCGGGCGCTTCGCGGGCAGAGAG 680
 TGGTACTACGGGAACGTGACGCGGCACCAGGCCGAGTGCG 720
 CCCTCAACGAGCGGGGCGTGGAGGGCGACTTCCTCATTAG 760
 GGACAGCGAGTCCTCGCCCAGCGACTTCTCCGTGTCCCTT 800
 AAAGCGTCAGGGAAGAACAACACTTCAAGGTGCAGCTCG 840
 TGGACAATGTCTACTGCATTGGGCAGCGGCGCTTCCACAC 880
 CATGGACGAGCTGGTGGAACTACAAAAAGGCGCCCATC 920
 TTCACCAGCGAGCACGGGGAGAAGCTCTACCTCGTCAGGG 960
 CCCTGCAGTGA 971 (SEQ ID NO:197)

FIG. 62

GAATTCGTCGACCCACGGTCCGAAATATAACTGAAGTTGGGGCACCTACTGAAGAAGAGGAAGAAAGTG	70
+++++	
E F V D P R V R N I T E V G A P T E E E E E S	23
+++++	
AAAGTAAGATAGTGAAGACAGTGGTGGGGAGCAAGAAGATGCAGAGGAGGAAGAGAAAGAGGA	140
+++++	
E S E D S E D S G G E E E D A E E E E E E K E E	47
+++++	
AAATGAATCTCACAAATGGTCAACCGGTGAAGAATACATCGCTGTTGGAGATTTTACTGCTCAGCAAGTT	210
+++++	
N E S H K W S T G E E Y I A V [G D F T A Q Q V	70
+++++	
GGAGATCTTACATTTAAGAAAGGGGAAATTCCTTGTAATTGAAAAAACCTGATGGTTGGTGGATAG	280
+++++	
G D L T F K K G E I L L V I E K K P D G W W I	93
+++++	
CTAAGGATGCCAAAGGAAATGAAGGTCTTGTTCCAGAACCTACCTAGAGCCTTATAGTGAAGAAGAAGA	350
+++++	
A K D A K G N E G L V P R T Y] L E P Y S E E E E	117
+++++	
AGGCCAAGAGTCAAGTGAAGAGGGCAGTGAAGAAGATGTAGAGGCGGTGGATGAAACAGCAGATGGAGCA	420
+++++	
G Q E S S E E G S E E D V E A V D E T A D G A	140
+++++	
GAAGTTAAGCAAAGAACTGATCCCCACTGGAGTGCTGTTTCAGAAAGCGATTTTCAGAGCGGGCATCTTTT	490
+++++	
E V K Q R T D P H W S A V Q K A I S E A G I F	163
+++++	

FIG.61A

GTCTTGTTAATCATGTCTCGTTTTGCTACCTAATAGTTCTGATCCGTCCTAA
+++++
C L V N H V S F C Y L I V L I R P 180
+++++

(SEQ ID NO:196)

FIG.61B

GAATTCGGCGGACTTCGCGGCCGCGTCGACGAAGAAACCTGAAGGACACACTAGGCCTCGGCAAGACGGC	70
I R R T S R P R R R R N L K D T L G L G K T R	23
CAGGAAGACCAGCGCGGGATGCGTCCCCACGCCACGACGGACGCCGAGTACCCCGCCAATGGCAGC	140
R K T S A R D A S P T P S T D A E Y P A N G S	46
GGCGCCGACCGCATCTACGACCTCAACATCCCGGCCTTCGTCAAGTTCGCCTATGTGGCCGAGCGGGAGG	210
G A D R I Y D L N I P A F V K [F A Y V A E R E	69
ATGAGTTGTCCCTGGTGAAGGGTCCGCGCTCACCGTCATGGAGAAGTGCAGCGACGGTTGGTGGCGGGG	280
D E L S L V K G S R V T V M E K C S D G W W R G	93
CAGCTACAACGGGCAGATCGGCTGGTTCCCTCCAACCTACGTCTTGGAGGAGGTGGACGAGGCGGTTGGC	350
S Y N G Q I G W F P S N Y] V L E E V D E A V A	116
GAGTCCCCAAGCTTCCTGAGCCTGCGCAAGGGCGCCTCGCTRGAGCAATGCCAGGGCTCCCGCGTGCTGC	420
E S P S F L S L R K G A S L S N G Q G S R V L	139
ATGTGGTCCAGACGCTGTACCCCTTCAGCTCAGTCACCGAGGAGGAGCTCAACTTCGAGAAGGGGGAGCAC	490
H V V Q T L [Y P F S S V T E E E L N F E K G E T	163

FIG.63A

```
CATGGAGGTGATTGAGAAGCCGGAGAACGACCCCGAGTGGTGGAAATGCAAAAATGCCCGGGCCAGGTG
|-----| 560
M E V I E K P E N D P E W W K C K N A R G Q V 186
|-----|
GGCCTCGTCCCCAAAACTACGTGGTGGTCCTCAGTGACGGGCTGCCCTGCACCCTGCGCACGCCCCAC
|-----| 630
G L V P K N Y] V V V L S D G P A L H P A H A P 209
|-----|
AGATAAGCTACACCGGGCCCTCGTCCAGCGGGCGCTTCGCGGGCAGAGAGTGGTACTACGGGAACGTGAC
|-----| 700
Q I S Y T G P S S S G R F A G R E W Y Y G N V T 233
|-----|
GCGGCACCAGGCCGAGTGGCCCTCAACGAGCGGGCGTGGAGGGCGACTTCCTCATTAGGGACAGCGAG
|-----| 770
R H Q A E C A L N E R G V E G D F L I R D S E 256
|-----|
TCCTCGCCCAGCGACTTCTCCGTGTCCCTTAAAGCGTCAGGAAGAACAACACTTCAAGGTGCAGCTCG
|-----| 840
S S P S D F S V S L K A S G K N K H F K V Q L 279
|-----|
TGGACAATGTCTACTGCATTGGGCAGCGGCGCTTCCACACCATGGAGGAGCTGGTGGAACTACAAAAA
|-----| 910
V D N V Y C I G Q R R F M T M D E L V E H Y K K 303
|-----|
GGCGCCCATCTTCACCAGCGAGCACGGGGAGAAGCTCTACCTCGTCAGGGCCCTGCAGTGACGGCGCCCC
|-----| 980
A P I F T S E H G E K L Y L V R A L Q /322
|-----|
```

(SEQ ID NO:198)

FIG.63B

GAATTCGCGGACTTCGCGGCCGCGTCGACACCAGTGCAGG 40
TTTTGGAATATGGAGAAGCTATTGCTAAGTTTAACTTTAA 80
TGGTGATACACAAGTAGAAATGTCCTTCAGAAAGGGTGAG 120
AGGATCACACTGCTCCGGCAGGTAGATGAGAACTGGTACG 160
AAGGGAGGATCCCGGGGACATCCCGACAAGGCATCTTCCC 200
CATCACCTACGTGGATGTGATCAAGCGACCACTGGTGAAA 240
AACCCCTGTGGATTACATGGACCTGCCTTTCTCCTCCTCCC 280
CAAGTCGCAGTGCCACTGCAAGCCCACAGCAACCTCAAGC 320
CCAGCAGCGAAGAGTCACCCCGACAGGAGTCAAACCTCA 360
CAAGATTTATTTAGCTATCAAGCATTATATAGCTATATAC 400
CACAGAATGATGATGAGTTGGAACCTCCGCGATGGAGATAT 440
CGTTGATGTCATGGAAAAATGTGACGATGGATGGTTTGTT 480
GGTACTTCAAGAAGGACAAAGCAGTTTGGTACTTTTCCAG 520
GCAACTATGTAAACCTTTGTATCTATAA (SEQ ID NO:199)

FIG. 64

GAATTCGCGGACTTCGCGGCCGCTCGACACCAGTGCAGTTTTTGAATATGGAGAAGCTATTGCTAAGT	70
CTTAAGCGCCTGAAGCGCCGGCGCAGCTGTGGTCACGTCCAAAACCTTATACCTCTTCGATAACGATTCA	
ORF	
(E) F A D F A A A S T P V Q V L E Y G E A I A K	23
TTAACTTTAATGGTGATACACAAGTAGAAATGTCCTTCAGAAAGGTGAGAGGATCACACTGCTCCGGCA	140
AATTGAAATTACCACTATGTGTTTCATCTTTACAGGAAGTCTTTCCCACTCTCCTAGTGTGACGAGGCCGT	
F N F N G D T Q V E M S F R K G E R I T L L R Q	47
GGTAGATGAGAACTGGTACGAAGGGAGGATCCCGGGGACATCCCGACAAGGCATCTTCCCATCACCTAC	210
XXATCTACTCTTGACCATGCTTCCCTCCTAGGGCCCTGTAGGGCTGTTCCGTAGAAGGGGTAGTGGATG	
V D E N W Y E G R I P G T S R Q G I F P I T Y	70
GTGGATGTGATCAAGCGACCACTGGTGAAAACCTGTGGATTACATGGACCTGCCTTTCTCCTCCTCCC	280
CACCTACACTAGTTGGCTGGTGACCACTTTTTGGGACACCTAATGTACCTGGACGGAAGAGGAGGAGG	
V D V I K R P L V K N P V D Y M D L P F S S S	93
CAAGTCGCAGTCCCACTGCAAGCCCACAGCAACCTCAAGCCCAGCAGCGAAGAGTACCCCCGACAGGAG	
GTTACCGGTCACGGTGACGTTGGGTGTCGTTGGAGTTCGGGTCGTCGCTTCTCAGTGGGGGCTGTCCTC	350
P S R S A T A S P Q Q P Q A Q Q R R V T P Q R S	117

FIG.65A

TCAAACCTCACAAGATTTATTTAGCTATCAAGCATTATATAGCTATATACCACAGAATGATGATGAGTTG 420
AGTTTGGAGTGTTCTAAATAAATCGATAGTTCGTAATATATCGATATATGGTGTCTTACTACTACTCAAC
SH3
Q T S Q D L F S Y Q A L [Y S Y] I P Q N D [D E L] 140
GAACTCCGGATGGAGATATCGTTGATGTCATCGAAAAATGTGACGATGGATGGTTTGTGGTACTTCAA 490
CTTGAGGCGCTACCTCTATAGCAACTACAGTACCTTTTTACACTGCTACCTACCAAACAACCATGAAGTT
F
E L R D G D I V D V M E K C D D G [W F] V G T S 163
GAAGGACAAAGCAGTTTGGTACTTTCCAGGCAACTATGTAAACCTTTGTATCTATAAGAAGACTGAAA 560
CTTCCTGTTTCGTCAAACCATGAAAAGGTCCGTTGATACATTTTGGAAACATAGATATTCTTCTGACTTT
STOP
R R T K Q F G T F [R G N Y] V K P L Y L () 181
(SEQ ID NO:200)

FIG.65B

AATTCAAGCGCGGGTCTTTAGGATTTGCAGCTCCAGGAAGCGAGATGTCGAAGCGCCACCCAAACCA
+++++ 70

N S S A G S L G F A A P G S E M S K P P P K P
+++++

GTCAAACCAGGGCAAGTTAAAGTCTTCAGAGCCCTGTATACGTTTGAACCCAGAACTCCAGATGAATTAT
+++++ 140

V K P G Q V K V F R A L Y T F E P R T P D E L
+++++

ACTTTGAGGAAGGTGATATTATCTACATTACTGACATGAGCGATACCAATTGGTGGAAAGGCACCTCCAA
+++++ 210

Y F E E G D I I Y I T D M S D T N W W K G T S K
+++++

AGGCAGGACTGGACTAATTCCAAGCAACTATGTGGCTGAGCAGGCAGAATCCATTGACAATCCATTGCAT
+++++ 280

G R T G L I P S N Y V A E Q A E S I D N P L H
+++++

GAAGCAGCAAAAAGAGGCAACTTGAGCTGGTTGAGAGAGTGTTTGGACAACAGAGTGGGTGTTAATGGCT
+++++ 350

E A A K R G N L S W L R E C L D N R V G V N G
+++++

TAGACAAAGCTGGAAGCACTGCCTTATACTGGGCTTGCCACGGGGCCACAAAGATATAGTGGAAATGCT
+++++ 420

L D K A G S T A L Y W A C H G G H K D I V E M L
+++++

ATTACTCAACCAAATATTGAACTGAACCAGCAGAACAAGTTGGGAGATACAGCTTTGCATGCTGCTGCC
+++++ 490

F T Q P N I E L N Q D N K L G D T A L H A A A
+++++

FIG.66A

TGGAAGGGTTATGCAGATATCGTCCAGTTGCTTCTGCCAAAAGGTGCTAGAACAGACTTAAGAAACATTG
560
W K G Y A D I V Q L L L A K G A R T D L R N I
AGAAGAAGCTGGCCTTCGACATGGCTACCAATGCTGCCTGTGCATCTCTCCTGAAAAAGAAACAGGGAAC
630
E K K L A F D M A T N A A C A S L L K K K Q G T
AGATGCAGTTCGAACATTAAGCAATGCCGAGGACTATCTCGATGATGAAGACTCAGATTAA
D A V R T L S N A E D Y L D D E D S D ^{STOP}
^

(SEQ ID NO:221)

FIG.66B